

1
TCG ACT ATG AAT GCG GAT AGC GGT CGA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATG GGC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121
AGA GTA CCC GCG AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA GTG GGT GGT GCG
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT CTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser gln val gln arg lys ala val ser ala ile his

241
AGC CTG CTA AGT TCT CAC CAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG CTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301
ATC GCC GCG CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601
CTC ATT AGG AAG TGG ATT GCT CAG CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661
CTT TTT ATT TGT CCG TTA TCT TTT CAG TAT AAG GAA AAA CAG AAT TTT CAA AAA GTT ATT
leu phe ile tyr val leu tyr phe gln tyr lys gln lys gln ser ser asp lys val ser

721
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCG GGG CTG GAA GAG GGT TTG CTG GGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781
GGG GAA GGG GGT AAA TGG CAG AAT ATG GCG TGC CCG GGT CCA GCG AAC GAC CGA TTT CTA

FIG. 1 (1 of 5)


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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
AAC AAG CTA AAA GAG AAC CTC AAG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAC
asn lys leu lys gln asn leu arg pro met ile gln arg lys ile pro glu leu tyr lys

1881
TCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAT TCC TTC TAC AGA TCT AGT TTT AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser pheHis arg ser ser phe arg lys

1941
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA CAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser CCH glu lys pro ser ser phe val glu thr val

1971
GGC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GGC ACC CAG
ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln

2061
GAC TGA CTG TAC ACT CCC TGA TCA GGC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA
asp STP

2121
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ACT TTT GCC ATA CTG GGG GGT GGC GGG ATG

2131
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

2241
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CCG GCC AAT CAC TGC CCA TCT GAG AGA TGA

2301
TTT CCT CTG GGC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

2331
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

2421
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

2481
AAA TCA TCA TGC TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

2541
ATG GTG GAG TAA TTT CTG TAT AGT TAT TTT TGT TTT ATT ACT ACT GTT ACA TTA ATT TAA

261
TAT TTA TTT ATA TAA TAA TAT ATT TAA AAT AAT TAT TTA TTA GAT TTA TTA TAT TTG GAG

2661
CAG TCA GGC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAG AAT TCT CCG ATA ATG

2731
CTT TGC TCT TTT TCT TAT GTG ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

2761
AAT TTT TTT TTA TAA AAT AAT AAT AAT TAT TTT TTT ATT TTA TAA TAT TGT GGT CTT TTT

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FIG. 1 (4 of 5)

4021
AAC TCG

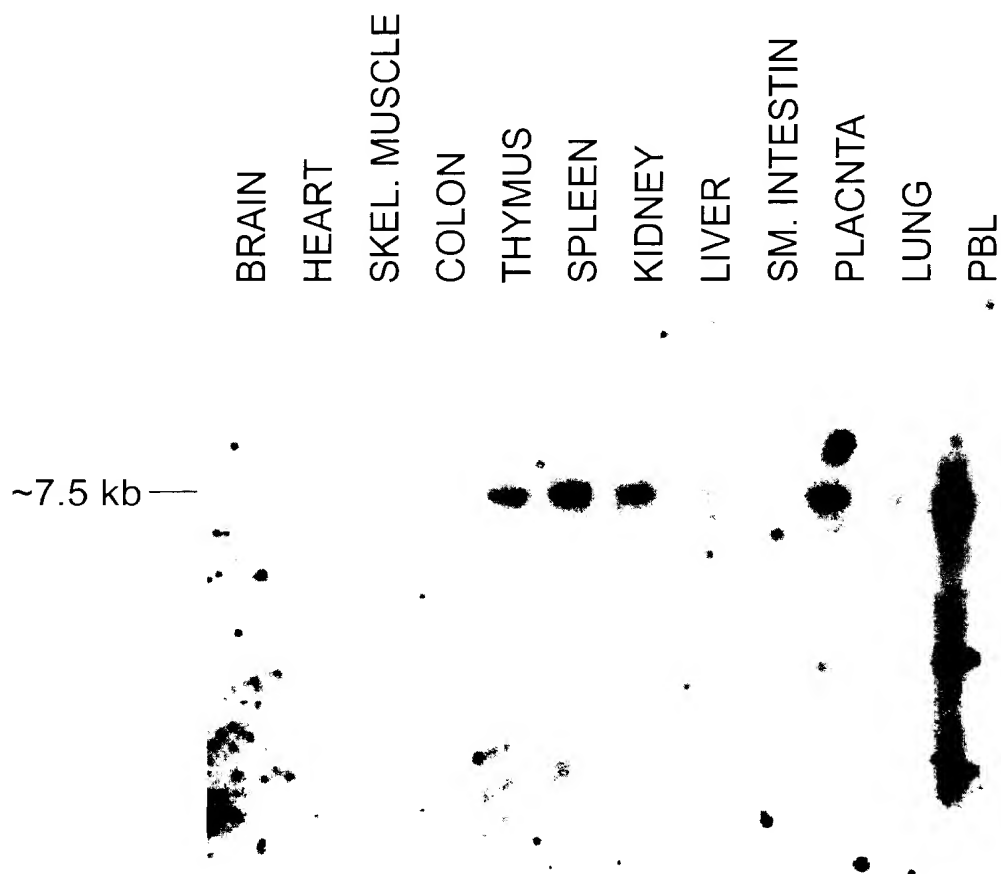


FIG. 2A

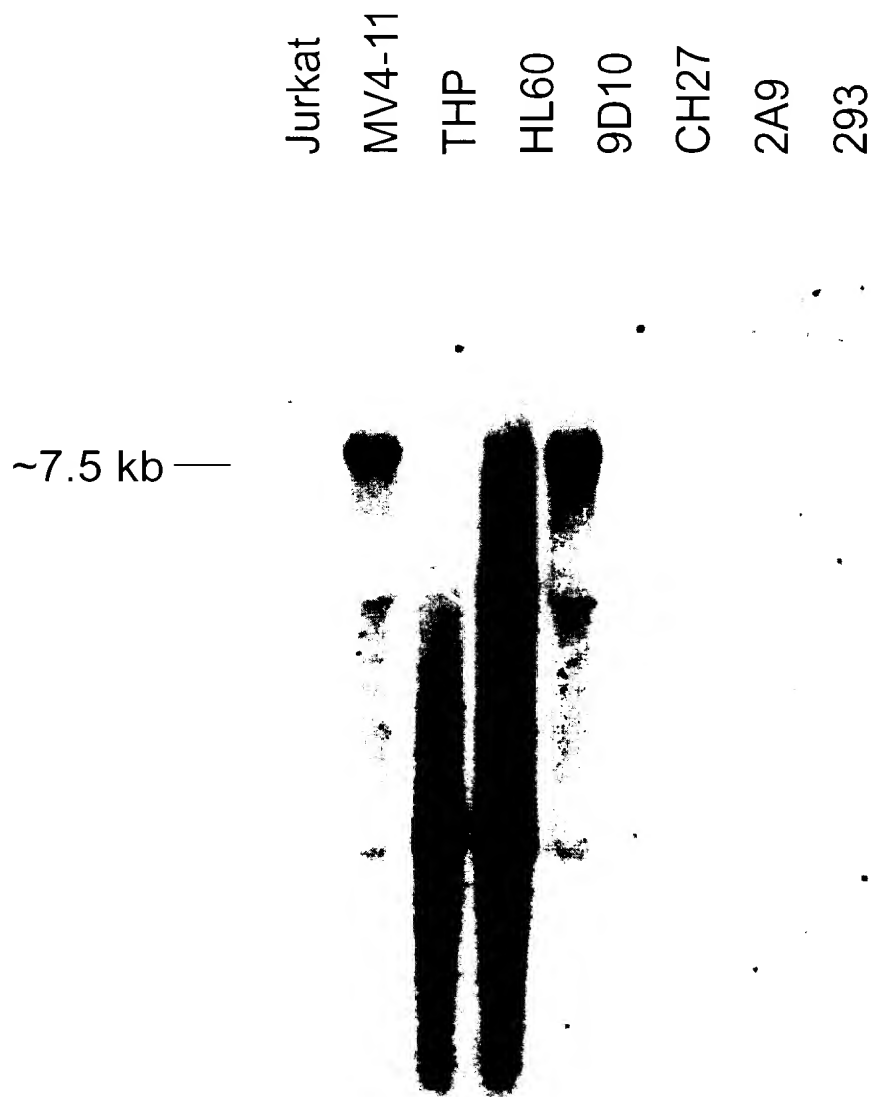


FIG. 2B

HC2A -----
 KIAA ASGNLDKNARFSAIYRQDSNKLSNDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----
 KIAA FPNVYNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLVYFKYLKYDSQ
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----VLHHQNPFFYDEIK
 KIAA KSFAKARNIALCIEFKDSDEEDSQPLLCIYGRFGGPVETRSAFAAVLHEHQNPFFYDEIK
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----
 KIAA IELPTQLHEKHALLLTFFHVSCDNSSFGSTKKFDVWETQVGYSWLPLLDGAVVTSECHI
 rat IELPTQLHEKHALLLTFFHVSCDNSSFGSTKKFDVWETQVGYSWLPLLDGAVVTSECHI
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----
 KIAA PVSANLPSGYLGYGELGMGEHYGPEIFWVDGCKPLLKIISTHLVSTVYTQDCHLHNFETYC
 rat PVSANLPSGYLGYGELGMGEHYGPEIFWVDGCKPLLKIISTHLVSTVYTQDCHLHNFETYC
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----
 KIAA QRIECSAIALDNELVYLRSLHAMEGSHVIAFLDVIINLPSAVLT-RATQELVAVNVIRV
 rat LPTFCVIALDNELVYLRSLHAMEGSHVIAFLDVIINLPSAVLT-RATQELVAVNVIRV
 HC4 -----NEIQVLIREFLSVILMQLFWVLPNMIHEIDVPISCFMV
 HC1 -----MSFLPIILNQLFKVLV-QNEEDSLTTTVIRV
 HC3 NRSRNLNSNSNFDISGTFSTSPDDEVRSITGSKGLDRGNSKVNVTGGPKAAPWGNPSPSAKS
 HC5 -----

FIG. 3A (1 of 5)

HC2A 11HVVAQCCHEEGLESHLSRYVHYAYKAEPYVASEYKTVHEELTKSMTTILPSPADFLTSN
 KIAA 11HVVAQCCHEEGLESHLSRYVYATMAEPYVASEYKTVHEELTKSMTTILNPSADFLTSN
 rat -----
 HC4 LFHIVSKCHEEGGLDLYLSSFIKYSIFFGKHSAPQAPLIHETLATNMIALLIQSADFLAIN
 HC1 LPDITAKCHEEQQLDSVYSYIFVVIKTR---ACKERPVEDLARNVTGLIF--SNDSPTVK
 HC3 TQAMPDSNCRNMSSTETESFLQTLTGRLP---TKKLPHHEELALQWVVCSG--SVF---E
 HC5 -----

Cadherin
Cleavage

HC2A KLLRYSWFFFDVLIISMAQHLIENSHVHLIANDPFPASYHHAABETVMNMLMPHITQKFGD
 KIAA KLLRYSWFFFDVLIISMAQHLIENSHVHLIANDPFPASYHHAABETVMNMLMPHITQKFRD
 rat -----
 HC4 KLLRYSWFFFEIISMAQHLIENSHVHLIANDPFPASYHHAABETVMNMLMPHITQKQAE
 HC1 HVLLHSWFFFAIILISMAQHLIDTNFIQLIPQREPERVQNELDNLVMDLADHVIWVYKD
 HC3 SALQQAWFFFEIMVFSMTHHLIENDLEAFKSRFPPIFMDIDIAALNSTIASDVSRIQK
 HC5 -----

HC2A NPEALKNANHSLAVFIHRCFTFMDRGVFFQIN---NYSIS--CPAPGDPETLFEYIFLFL
 KIAA NPEALKNANHSLAVFIHRCFTFMDRGVFFQIN---NYSIS--CPAPGDPETLFEYIFLFL
 rat -----
 HC4 IPRKSRVNVYSLAFILHCLTLMDRGCVFVFLIN---DYSIS--GEPPIPKVLANVYIFLFL
 HC1 ALRECRRAITHSVARILHRCFTFMDRGCVFFMVN---NYSIS--MFSGILKTLQGVFDEL
 HC3 DTEMVERLNTSLAFILNDLLSVMDRGCVFSLIKSCYKQVSSKLYSLNPSVLVSLILDEL
 HC5 -----

HC2A RVVCHHEHYIPLNLLM-----FPGFGRIQF-----VQDQL-----DYSITDEF
 KIAA RVVCHHEHYIPLNLLM-----FPGFGRIQF-----VQDQL-----DYSITDEF
 rat -----
 HC4 QTICNHEHYIPLNLLM-----AFAPFRIQF-----VQDNL-----EYVISLEY
 HC1 QEVCCQHEHFIPCLDIHGANIFDPIFSES-----TQELHASTMPETVVTNEF
 HC3 RYICSHHEHYVTLNLPCLLTTPASISSESVSSATSQSSCFSTN'QDQFIANMFELE--VPE
 HC5 -----MADTAFTSICFESIS---SQNSLSCSSPQDQFIASHFDRTFVPA

Cadherin
EC motif

HC2A CRNHFLVGLLRLR'GTALQEFFE---VRLIAISVLNLLIKHSFDRYASRSHQARIAT
 KIAA CRNHFLVGLLRLR'GTALQEFFE---VRLIAISVLNLLIKHSFDRYASRSHQARIAT
 rat -----
 HC4 CRNHFLVGLLRLR'GTALQEFFE---VRLIAISVLNLLIKHSFDRYASRSHQARIAT
 HC1 CRNHFLVGLLRLR'GTALQEFFE---VRLIAISVLNLLIKHSFDRYASRSHQARIAT
 HC3 CRNHFLVGLLRLR'GTALQEFFE---VRLIAISVLNLLIKHSFDRYASRSHQARIAT
 HC5 CRNHFLVGLLRLR'GTALQEFFE---VRLIAISVLNLLIKHSFDRYASRSHQARIAT

HC2A NYLFLVGLLIRNVQRINVRDVSPPFVAG-MTVFDESALAPANNPLVTPQKGSTLNSLH
 KIAA NYLFLVGLLIRNVQRINVRDVSPPFVAG-MTVFDESALAPANNPLVTPQKGSTLNSLH
 rat -----
 HC4 NYLFLVGLLIRNVQRINVRDVSPPFVAG-MTVFDESALAPANNPLVTPQKGSTLNSLH
 HC1 NYLFLVGLLIRNVQRINVRDVSPPFVAG-MTVFDESALAPANNPLVTPQKGSTLNSLH
 HC3 NYLFLVGLLIRNVQRINVRDVSPPFVAG-MTVFDESALAPANNPLVTPQKGSTLNSLH
 HC5 NYLFLVGLLIRNVQRINVRDVSPPFVAG-MTVFDESALAPANNPLVTPQKGSTLNSLH

FIG. 3A (2 of 5)

H22A KELLGATSGIASPYTTSTFNINYNRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
 K1AA KELLGATSGIASPYTTSTFNINYNRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
 rat -----
 H24 TDKDTATGSSPQNS-----H3IKREDNRSSLIP-EGATSPDQGTNGEN-----TRQS
 H21 KDWLNSIAAFSP-----IATSTFTHALSHASLASLGNPSTNFKSSBKIDNCEKIPRPL
 H23 EIVANALAGTSVI-----LTAPGSELTSTSRQHT-----
 H25 QNVALAIAQNNFN-----LETSGLIVLSSLP(EQYN)-----

 H22A TLGNSVTHKDRILDQSEIKSLMCHLVILEKMSDDALFTYWN-KASTSELMDFFTIGEVCL
 K1AA TLGNSVTHKDRILDQSEIKSLMCHLVILEKMSDDALFTYWN-KASTSELMDFFTIGEVCL
 rat -----
 H24 STRSSVYQYNRLDQVEIRSLNCHLVIVPHISEDTLLTYWN-KVSPQELNINILILEVCL
 H21 ALIGSPLHFDRLDQAETRSLMCHLVIMETISYETLIAYWQ-RAPSPVSDFFSILDACL
 H23 -----TFSAESSRSLICMLWVLEN-ADET/LQKWFTDLSVLQNLRLDLILYLV
 H25 -----MINADTTRNMLCHLVIMEN-ADQSLIRKWADLPSTILNRLDLILYLV

 H22A HQEQYDGFYIAHQEGLG--PIVHIRE-----[TLPVSENIETGM
 K1AA HQEQYDGFYIAHQEGLG--PIVHIRE-----[TLPVSENIETGM
 rat -----
 H24 FHEFIMPFENIAPVHDAWLSKRFGLIRHC-----[THPALENSGWM
 H21 QNFEVLGKRNIIETAAAF--EFVQSTQNDGTLKGSNPSC[TSGLIAIWMHSTIRREGHK
 H23 SCFELVGFYVFEFHNLSLTFK--KRFIMAR-----LHEALGSGIAPQENT
 H25 LCFELVGFQCSDFVSTQVLQ--KRFIVFAE-----LFEALLRGEGAFGEMH

 H22A HARELQQL-----GSLDMS-----LTFNHSYGHVADAVLHQSLLEANIATEVC
 K1AA HARELQQL-----GSLDMS-----LTFNHSYGHVADAVLHQSLLEANIATEVC
 rat -----
 H24 QARELQQL-----SSLENS-----FTLNHSSTITEADLPHQALLEGNTATEVC
 H21 QHRSQCLIIIRGK---NALSMPRL---ICMLICMTISNSNEIDIVHHVDTEANIATEVC
 H23 RRSFQQLFELPSGLAFGSQENILWFEDNTHWRQITEKLDKFAELIHEALIDGNLATEAN
 H25 RREAFGNHFFP-----GLNENLAWFEQTHWRQANEKLDKFAELDQEAIDGNLATEAN

 H22A LTALQTLISIFTLAFENQLLADHGHNILNFFVFIWYLCFLQHQHQBETALKNVFTALFSLIY
 K1AA LTALQTLISIFTLAFENQLLADHGHNILNFFVFIWYLCFLQHQHQBETALKNVFTALFSLIY
 rat -----
 H24 LTVLQTLISIFTQCHETHFLNHDGHNELNFFVFIWYLCFLQHQHQBETALKNVFTALFSLIY
 H21 LTILQTLISIFTQTHGRQLQQCDQNSLNHGFQCYMLFFQVQNSATALKHVFAELFLVQ
 H23 LIILQTLISIVQTVS--VTEL--LESILGGVILYLLHSMACNQSAYVLOHCFATQRAIM
 H25 LIILQTNENIQALS--ALDC--KPSILGGVILYLVNLSNMDQSTCTYLHCFATLRLIA

 H22A KFFSTFVFPAIMAAALVYELDGNCHLNTIPEASQLLFLMRNFEYTKKRFELIETH
 K1AA KFFSTFVFPAIMAAALVYELDGNCHLNTIPEASQLLFLMRNFEYTKKRFELIETH
 rat -----
 H24 KFFSAFFHGRVNMIAAFQYVNLKCTSIISTINEASALLFLMRNFEYTKKRFELIETH
 H21 KFFSAFFHGRVNMIAAFQYVNLKCTSIISTINEASALLFLMRNFEYTKKRFELIETH
 H23 KFPPELLFEEETEQQADLCLRLRHCSSTICTIFHPSASINLLMRNFEYTKKRFELIETH
 H25 KFGMLLFEFEEVQTHDLCHQLHHCSSMDVTFQACATLALLMRNFEYTKKRFELIETH

H22A LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 K1AA LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 rat -----
 H24 LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 H21 LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 H23 LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 H25 LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM

H22A LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 K1AA LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 rat -----
 H24 LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 H21 LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 H23 LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM
 H25 LQVITISVSDLIADVWVGIFETFEICSLGIIINCAVSDPLIKHTSFSDDVKPLTERIRIVIM

HC2A	ATAQNHKEHENDPEMLVDLQYSLAKSTASTPELRKTHLDSMARHIFKNGDLSSEAAACGVVHV
PIAA	ATAQNHKEHENDPEMLVDLQYSLAPSTASTPELITKTHLDSMARHIFKNGDLSSEAAACGVVHV
1a1	ATAQNHKEHENDPEMLVDLQYSLAKSTASTPELRKTHLDSMARHIFKNGDLSSEAAACGVVHV
HC4	ATAQNHKEHENDPEMLVDLQYSLAKSTASTPELRKTHLDSMARHIFKNGDLSSEAAACGVVHV
HC1	ATAQNHKEHENDPEMLVDLQYSLAKSTASTPELRKTHLDSMARHIFKNGDLSSEAAACGVVHV
HC3	ATAQNHKEHENDPEMLVDLQYSLAKSTASTPELRKTHLDSMARHIFKNGDLSSEAAACGVVHV
HC5	DTVNRHREHQEDPEMLDLMYRIAKSGQTSFDLRLTLQLNNAAGHSLERSHAEAAACLVHS

HORA TALVAEYLKREKV-----PQSTAFMVTEN
 KIAA TALVAEYLKREK-----VQVEPLLPRSHADLRKSGGVTRQSTAFMVTEN
 rat TALVAEYLKREKAD-----LALDEPPVVP:SHTSCKKSG:GIRFFPQSTAFMVTEN
 HCL AALVAEYLKREKL-----FINGSAFVKLEN
 HCL AALVAEYLKREKVKERIGTAALLREVTHTPDSNALLTTPSGGIMFNSGWPAPFSTEN
 HCL AALVAEYLKREK-----RYLNGGVTHNHNEN
 HCL AALVAEYLKREK-----HCLLVSVSEPHLEN

ITAM

KC2A	IDEASNNILVGMQD-----VHFNELVLMELLI	CADGLWFAHRE	ELLADIYF	11	PI
KIAA	IDEASNNILVGMQD-----VHFNELVLMELLI	CADGLWFAHRE	ELLADIYF	11	PI
rat	IDEASNNILVGMQD-----VHFNELVLMELLI	CADGLWFAHRE	ELLADIYF	11	PI
KC4	IDEASNNILVGMQD-----VHFNELVLMELLI	CADGLWFAHRE	ELLADIYF	11	PI
KC1	IDEASNNILVGMQD-----VHFNELVLMELLI	CADGLWFAHRE	ELLADIYF	11	PI
KC3	IDEASNNILVGMQD-----VHFNELVLMELLI	CADGLWFAHRE	ELLADIYF	11	PI
KC5	IDEASNNILVGMQD-----VHFNELVLMELLI	CADGLWFAHRE	ELLADIYF	11	PI

	ITAM	ITAM	ITAM	ITAM
HCPA	LENIPLD			
KIAA	TEKRFDFPLARD	ITITREASSPT	TEVNIHSGRFLD	TEFMAFFGQAAQYQFTILRTQVE
rat	EMRGGTATETTR	ITITREPSYR	TEVITR	-----A-----AGWDLLFGGLGNG
H04	LENLEFENLTQV	ETLHGAST	TELVNHTKEFLDG	-----TEFMAFENG
H07	PERQDFPLLED	YDHSRSLP	AFVNSEFLDFG	-----RAYENFENG
H03	HEANDAFPL	LTTHGFLQAF	EFVHQSGTWEEMN	-----TEFNGTENG
H05	LEAHEKPL	LTLTSLKQAF	EFVTVNKLH	-----TEFNGTENG

[illegible]

HTAA YVQVTHVIVFFDEKEIQRKTEFEERCHNIRLEMFEMPITQTGIIQGSWEEQCHFTILTA
 KIAA YVQVTHVIVFFDEKEIQERKTEFEERSHNIRLEMFEMPITQTGIIQGSWEEQCHFTILTA
 rat YVQVTHVIVFFDEKEIQERKTEFEERCHNIRLEMFEMPITQTGIIQGSWEEQCHFTILTA
 H14 YVQVTHVIVFFDEKEIQERKTEFEERCHNIRLEMFEMPITQTGIIQGSWEEQCHFTILTA
 H01 YVQVTHVIVFFDEKEIQERKTEFEERCHNIRLEMFEMPITQTGIIQGSWEEQCHFTILTA
 H03 YVQVTHVIVFFDEKEIQERKTEFEERCHNIRLEMFEMPITQTGIIQGSWEEQCHFTILTA
 H04 YVQVTHVIVFFDEKEIQERKTEFEERCHNIRLEMFEMPITQTGIIQGSWEEQCHFTILTA

FIG. 3A (4 of 5)

Coiled-Coil 1

HC2A	IHCFPTVYFRIPVMYQHHTDLNFI	EVVAIDEMSKVVAELRQLCSSAEVDMIKLQLHQQSSV
KIAA	IHCFPTVYFRIPVMYQHHTDLNFI	EVVAIDEMSKVVAELRQLCSSAEVDMIKLQLHQQSSV
rat	IHCFPTVYFRIPVMYQHHTDLNFI	EVVAIDEMSKVVAELRQLCSSAEVDMIKLQLHQQSSV
HC4	SNSEFTVYFRIPINCEQQINLKEI	DGATDELRKVAELQQLCSSAEVDMIKLQLHQQSSV
HC1	SHLFPVYKKRIQVLSQSSTELNFI	EVVAIDEMSKVVAELRQLCSSAEVDMIKLQLHQQSSV
HC3	SHAFPTVYFRIPVYTHKEEII	ILTPFEVAIEDMQKRTQELAFATHQDPADPKNLQMVVLOQSSV
HC5	SHAFPTVYFRIPVYTHKEEII	ILTPFEVAIEDMQKRTQELAFATHQDPADPKNLQMVVLOQSSV

Coiled-Coil 2

HC2A	SVQVNAGPLAIAAFELDDTNTFRYPDNKVLLI	EVFFQFVEACGGQALAVNERLIFEDQLE
KIAA	SVQVNAGPLAIAAFELDDTNTFRYPDNKVLLI	EVFFQFVEACGGQALAVNERLIFEDQLE
rat	SVQVNAGPLAIAAFELDDTNTFRYPDNKVLLI	EVFFQFVEACGGQALAVNERLIFEDQLE
HC4	SVQVNAGPLAIAAFELNDSQASLYPPKKVSELI	DMFFKFIQACSIALLINEFLIFELQVE
HC1	SVQVNAGPLAIAAFELNDSQASLYPPKKVSELI	DMFFKFIQACSIALLINEFLIFELQVE
HC3	SVQVNAGPLAIAAFELNDSQASLYPPKKVSELI	DMFFKFIQACSIALLINEFLIFELQVE
HC5	SVQVNAGPLAIAAFELNDSQASLYPPKKVSELI	DMFFKFIQACSIALLINEFLIFELQVE

Coiled-Coil 2

HC2A	EQEELFANYFEMAKELSEIMHEDLG	CELEHETS-VLPNLSHIFNAISGIPTSIMVHGMTSS
KIAA	EQEELFANYFEMAKELSEIMHEDLG	CELEHETS-VLPNLSHIFNAISGIPTSIMVHGMTSS
rat	EQEELFANYFEMAKELSEIMHEDLG	CELEHETS-VLPNLSHIFNAISGIPTSIMVHGMTSS
HC4	EQEELFANYFEMAKELSEIMHEDLG	CELEHETS-VLPNLSHIFNAISGIPTSIMVHGMTSS
HC1	EQEELFANYFEMAKELSEIMHEDLG	CELEHETS-VLPNLSHIFNAISGIPTSIMVHGMTSS
HC3	EQEELFANYFEMAKELSEIMHEDLG	CELEHETS-VLPNLSHIFNAISGIPTSIMVHGMTSS
HC5	EQEELFANYFEMAKELSEIMHEDLG	CELEHETS-VLPNLSHIFNAISGIPTSIMVHGMTSS

P-M

HC2A	CVTLPHPEPHVGTCEVVMCKLRRTFFANHHWFCQAQEEAMGNGREKEPWTVIFNSRFYFSWCK
KIAA	CVTLPHPEPHVGTCEVVMCKLRRTFFANHHWFCQAQEEAMGNGREKEPWTVIFNSRFYFSWCK
rat	CVTLPHPEPHVGTCEVVMCKLRRTFFANHHWFCQAQEEAMGNGREKEPWTVIFNSRFYFSWCK
HC4	CVTLPHPEPHVGTCEVVMCKLRRTFFANHHWFCQAQEEAMGNGREKEPWTVIFNSRFYFSWCK
HC1	CVTLPHPEPHVGTCEVVMCKLRRTFFANHHWFCQAQEEAMGNGREKEPWTVIFNSRFYFSWCK
HC3	CVTLPHPEPHVGTCEVVMCKLRRTFFANHHWFCQAQEEAMGNGREKEPWTVIFNSRFYFSWCK
HC5	CVTLPHPEPHVGTCEVVMCKLRRTFFANHHWFCQAQEEAMGNGREKEPWTVIFNSRFYFSWCK

HC2A	-----
KIAA	-----
rat	VHIF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

FIG. 3A (5 of 5)

[illegible]

TRG PKLTPLSEL SQFLHLHYSDHFESEN¹FIHQDSFVWTF¹ILLSKFAY¹IQVTHVTPFFFEKE
 CLASP-1 PKLTGLSEL SQFLHLHYADHFAWNV¹FIHQDSFVWTF¹ILLSKFAY¹IQVTVYTPFFFEKE
 CLASP-2 PKLTPLSEL SQFLHLHYSDHFESEN¹FIHQDSFVWTF¹ILLSKFAY¹IQVTHVTPFFFEKE
 CLASP-4 PKLTGLSEL SQFLHLHYGKFTTENVA¹FIHQDSFVWTF¹ILLSKFAY¹IQVTVYTKVPFFFEKE
 CLASP-3 PAITFLAEL IFFLEGFYCKKREEDV¹EVIRKDSNV¹FIQLPNKAY¹IQVITYVEPYFDIYE
 KIAA0716 HDYEFLEAFQGMLEFFFAIA-----MQHAHQF¹ETFLAEAG¹YLIIYAV¹TPIPSEGE
 DOCK3 HDYEFLEAFQGMLEFFQAVAA-----MQHNH¹FIALLQDAQ¹YLIIYAV¹TPIRYVD
 DOCK2 PQMLNLTQFIDAKE-----INTTSAIG¹DVFNAPG¹YIICFTVQPVLDCHP
 DOCK180 EYREDEDFQMGLTQFPNAKH-----INTTSAIG¹DVFNAPG¹YIICFTVQPVLDCHP
 CONSENSUS L D Y Y Y Q+ V P D
 M E I E

	E										D									
CLASP-1	FTILDTTSNHFPPYV	FF	FI	QV	MS	QS	ST	SL	PI	EV	AI	EN	FF	YSEL						
TRG	ETILTIAIHGFPYV	FF	FI	IV	NT	QH	HT	IL	NI	EV	AI	EN	FF	YAEIL						
KIAA1058	ETILTIAIHGFPYV	FF	FI	IV	NT	QH	HT	IL	NI	EV	AI	EN	FF	YAEIL						
CLASP-2	ETILTIAIHGFPYV	FF	FI	IV	NT	QH	HT	IL	NI	EV	AI	EN	FF	YAEIL						
CLASP-6	ETILTIAIHGFPYV	FF	FI	IV	NT	QH	HT	IL	NI	EV	AI	EN	FF	YAEIL						
CLASP-4	ETILDTSNCFPPYV	FF	FI	IV	NC	FQ	IN	LE	DI	AT	DE	ET	DT	YAEIQ						
CLASP-3	ETILDTSHAFPPYV	FF	FI	IV	NT	QH	HT	IL	NI	EV	AI	EN	FF	YAEIL						
CLASP-5	NTVLITMHAFFPYI	ET	IS	VI	QV	EE	FVL	IT	EV	AI	EN	KFTIQLA								
KIAA0716	ETSLYLQSQSLPGI	SR	WF	FEM	ER	KK	EN	VEM	SL	EN	AI	EV	EN	NOQLK						
FOCK	RTSPVATYKLPGLI	SR	WF	FEM	ER	KK	EN	VEM	SL	EN	AI	EV	EN	TANKEKIL						
ETSPV	RTSPVATYKLPGLI	SR	WF	FEM	ER	KK	EN	VEM	SL	EN	AI	EV	EN	TANKEKIL						
ETSPV	RTSPVATYKLPGLI	SR	WF	FEM	ER	KK	EN	VEM	SL	EN	AI	EV	EN	TANKEKIL						
ETSPV	RTSPVATYKLPGLI	SR	WF	FEM	ER	KK	EN	VEM	SL	EN	AI	EV	EN	TANKEKIL						
ETSPV	RTSPVATYKLPGLI	SR	WF	FEM	ER	KK	EN	VEM	SL	EN	AI	EV	EN	TANKEKIL						

FIG. 3B (1 of 2)

CLASP-1	SLQLKLQGSMSVQVNAQPLAFAFAFLDDTNTHEYPONKV--KLLF	EIFRQFADACGGQALD
TRG	KLQLKLQGSMSVQVNAQPLAFAFAFLDDTNTHEYPONKV--KLLF	ENFRQFVEACGGQALA
KIAA1058	KLQLKLQGSMSVQVNAQPLAFAFAFLDDTNTHEYPONKV--KLLF	ENFRQFVEACGGQALA
CLASP-2	KLQLKLQGSMSVQVNAQPLAFAFAFLDDTNTHEYPONKV--KLLF	ENFRQFVEACGGQALA
CLASP-6	KLQLKLQGSMSVQVNAQPLAFAFAFLDDTNTHEYPONKV--KLLF	ENFRQFVEACGGQALA
CLASP-3	MLQMVLLQGSVGTUNQGPLEVAQVFLSE--IPSDPKLFLHHNKIL	LCFKDFTKRCEDALR
CLASP-4	QLQLKLQGSMSVQVNAQPLAFAFAFLDDTNTHEYPONKV--KLLF	ENFRQFVEACGGQALA
CLASP-5	MLQMVLLQGSVGTUNQGPLEVAQVFLSE--IPSDPKLFLHHNKIL	LCFKDFTKRCEDALR
KIAA0416	PLTMCLNGVLDAAVNGGVSRQQAFFEVKEYILSHPELGGKIAKIL	ELMLEDAQILEFGLA
DOCH2	PLSMILLNGIVDPAVNGGFATKFAFFETHEYVRIHPEDQKLTHIL	DLIAWQIPFLGAGIK
DOCH3	LLSMCLNGVIDAAVNGGIARQQAFFEDKDYINHPGDAEKITQLF	ELMQEDVHVLGVGLA
DOCH180	PLSMILLNGIVDPAVNGGFATKFAFFETHEYVRIHPEDQKLTHIL	DLIAWQIPFLAEGTR
CONSENSUS	L M L+G V VN G Y AFL + + P L+	L
	L I V V F +	I

DOCH2=KIAA0209
DOCH3=KIAA0299
CLASP2variant=KIAA1058

ref 1.1

↓

100 ACT ATG AAT GGT GAT AGT GGT GGA AAA TGT CCT TGT GGT TGG ATA TCT TCC CAG AAG
per thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

101

102 TTA AGT TTT TTT TTT ACC TTG CAG GAT CAG AAG ATC GGT AGG ATG TTT GAT CGG ACT TCC
per ser ser ser ser ser phe ala asp ala lys ile ala ser met phe asp arg thr ser

103

104 AGA GTA GGT GGT AGC AGC ACT TTC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

105

106 CTG GAT GGC GAA GGG GAA GGA ATC AGC GAA GCA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

107

108 AGC CTG CTA AGT TCT CAC GAC CTC GAC CCA GCG TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

109

110 ATC GCG GCG GGT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

111

112 GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC GCG ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

113

114 GGA GCG GGT GCG ATT ACC CAG AAT GTG GCT CTG GCG ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

115

116 AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCG TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

117

118 GAC AGT ACT GCG AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

119

120 CTC ATT AGC AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile ala lys trp ile ala gln pro ser thr gln leu asn arg ile leu asp leu

121

122 TTT TTG AAT TAT TTT TTA TTT TTT GAT TAT AAT TTA AAA CAG AAT TTT GAT AAA TTT AAT
leu phe ile thr val leu lys pro ala tyr lys gly lys gln ser ser asp lys val ser

123

124 AAT GAA TTT TTT CAG AAG TCA AGG GAT GTC AAG GCG GCG CTC GAA GAG GCT TTG CTG CGT
thr ala val leu gln lys ser arg asp val lys ala arg leu gln glu ala leu leu arg

125

126 TTT GAA TTT TTT AAT TTT GAT AAT AAT TTT TTT GAT TTT TTT TTT TTT TTT TTT TTT TTT
leu phe ala ala ala ala ala ala ala ala ala ala ala ala ala ala ala ala ala ala ala

FIG. 4A (1 of 7)

841
TGT CTA AAT GAA AAT TTT AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GGT AAT GAG
gly leu asp ala asp leu arg trp lys lys glu gln thr his trp arg gln ala asp gln

851
AAG CTA CAT AAA ATA AAG GGC GAG TTA CAT CAA GAA GGC TTG ATG AGT GGG AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

861
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG CGC AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val val asn ser leu asn

1061
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261
TAC CTC CTC ATG AGG TTC AGT TTT GAA GGC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441
TGT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro pro pro thr ala val ala ile leu leu cys asn leu asn ser ile leu tyr asp thr

1501
TTT AAA AAT AAT GAA TTT CAA CAA CAT TTT GAT AAT TTT ATG GAC CTT ATG TAT ACA ATT
val lys met arg ala pro gln ala asp pro gln asp leu met asp ile met tyr arg ile

1561
TGT AAG AGT TAT CAG GCA TTT CTT CAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621
AAA AAT AAT AAT AAT TAT TAT AAT TAT TTT TAT ATG TAT CTT CTT TAT AAT AAT AAT
lys ala ala ala ala thr thr ala thr thr thr thr thr thr thr thr thr thr thr thr thr

1681
TTA GTG GGT GAG TAT CTC AGC ATG CTG GAG GAC CAC AGC TAC CTC CCC GTG GGC AGT GTC
leu val ala gln tyr leu ser met leu ala asp his ser tyr leu pro val gly ser val

1741
AGC TTC GAG AAT ATT TCT TCC AAT CTC CTC GAG GAG TCT GTG GTC TCT GAG GAC AGC CTC
ser phe gln asp ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1801
TCA COT GAG GAG GAT GCG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTC GTA GGC
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861
CTC CTC GAG CAG GGT GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu ala gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GCG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2101
GAG CTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro
ref 4.1

2221
CTG GAT AAA ACT AAG TTC GAT TTT AAT AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp gln tyr ala met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341
GAG AGC GGT AAT TAT AAT ATT AAT TTT AAT TTT GAG GGT GGT GAT GAT GCA GAG CTC TAT
arg asp phe met tyr thr thr pro pro thr thr thr gly arg pro asp gly glu thr his

2401
GAG GAT GAT AAG AAG AAT ACA CTC CTC AAT ATT ATG TAC CTC TTC CCC TAC AAT AAG ACC
glu glu tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461
AAT ATT AAT TTT ATT TAT AAT AAT AAT TTT TTT TTT AAT TTT AAT TTT AAT TTT AAT TTT AAT
asp thr

FIG. 4A (3 of 7)

2571 2581
 GA⁺ ATG AAG AAG AA⁺ ATT TTS CAG TTA GCA GGT GGT ATT AAC CAG GAG CGG GGT GAT GCA
 asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

2591 2601
 AA⁺ AAG TTT AA⁺ ATT GAG TTA TAA TTT TTT TTA TTA ATT ATT GTA AAT CAG GGA GCA CTG
 lys met leu gln met val leu gln asp met val asp ala thr val asn gln gly pro leu

2611 2621
 GAA GTA GCC CAA GTG TTT TTG GGT GAA ATT GGT GGT GAT CCA AAA CTC TAT CGA CAT CAC
 glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2631 2641
 AAC AAG TTA AGG TTA TGG TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
 asn lys thr arg leu tyr phe lys glu phe ile met arg cys gly glu ala val glu lys

2651 2661
 AAC AAG CGT CTC ATC ACG GCA GAT CAG AGG TAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
 asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

2671 2681
 AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2691 2701
 CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
 pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2711 2721
 TGT GAA ACC CAG TTG TCA CAG GGG AGC TAA TAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
 cys glu thr gln leu ser gln cly ser och

2731 2741
 ref 5.1
 GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG

2751 2761
 GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA

2771 2781
 TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

2791 2801
 GAG GAT GAG TAC TCA GCG ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACT

2811 2821
 AAA TAA TTT AIA AAT AAT TTT TTT TTT TTA TTT AAA AAT TAT TAT TTA TAT GAG AAA TAA

2831 2841
 TTT TTT GGT AAT GAT ATT TTA ATT TAT TGT AAT AAT CAA AAT TTT CTG AGG AAA AAT GGA

2851 2861
 AAA ATT ATT CAG CAG TGG ATT CAA ACT GAA TTT CAC TCT TTA TAT GAA GGT AGG GCA AAC

2871 2881
 TTT TAT GAT TAT TAA AAA TTT TTA ATA AAT TTA TAA AAT TTA CTA CAA TTT CAA

FIG. 4A (4 of 7)

1541 AAA TCA TAA TTA TTA AAA ATT TTA GAA GAA ATT ATT TGT GAA GGT GTT AGG CTT TTG GTA
 1551 ATG GTG GAA TAA TTA GTG TAT AGT TAT TTT TTT TTT ATT ATT ATT GGT AGA TTA ATT TAA
 1561 CAT GCA TTT ATA GAA GAA TAC ATT GAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG
 1571 CAG TCA GGA AAA AAT CAG AGA TAC TGG TTT CAG TTA AAT GGA AAG AAT TGT CCG ATA ATG
 1581 GTT TGG TTT TTT TGT TAT GTG ACT GTT GTG TAC TAT GTA TTT TTT TCC TGT GTG GGA CCA
 1591 AGT TTT TTT TTA TAA AGT AAT AAT ATG TCT GTT TTT ATT TCA GAA CAT TGT GCT GTC TGT
 1601 CAG CAT ATG TAT ATG AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GSA CTT
 1611 TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT
 1621 GTG ACC TTG ACT GAT AAT AAA TAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA
 1631 AAC TCG

Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA. Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATACTTCCAGGTTATAAAAGNATTATTTACTAAAAGAANATTCANGC
TATTTTCATTTAACTAGCTCAGTTTAAATCATGTATTTCCTATAAAAGGTTAGTCTTATTAAT
TTGACAAAACAATCAAAACAATTCAAACCAGATCAAGTATGCTACCCCTGAAGTTACACC
ACTAGTTAAGAAATAACAATCTAAGTAATTTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA
TAACTTTAACTAAAGTCAAGAAATCCAAATAAGGCCCTATGAAATTTAGAAAATCATAGAA
AAATTCAAAATTTTCTTTTCTGAGATTAAGCAATTTGTTATATTAAGCAAAATAGAGGATT
AGAAATAAAATAATTTTGAAGCTGCTTTTACAGGTTTTTTCAGGCAAGCCCTCAAGAGCTT
AACTGGTTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG
TTCCAATNTTACTGGAACCCAGCAGTATCTTTNGAAGTCTTGATACTTAACCTGNGTGTA
CTCTCTTAAGGCTTANTANTAGCAATCTATATGATTTGTTGTTCTCTGNGCAAGNAG
 TGCCTATGAAA

Sequence of BA019 using primer H35A310b, which spans nucleotides 552-580 of Exon sequence is underlined and represents nucleotides 510-553.

224

Sequence of PAC14 using primer 3581, which spans nucleotides 106-1115 of the cDNA. Exon sequence is underlined and represents nucleotides 1118-1126.

 $\text{Fe} \in \text{A.L.}$

Sequence of F4C11 using primer Q5S7, which spans nucleotides 11-6-2205 of the cDNA. . Exon sequence is underlined and represents nucleotides 2245-2231.

[illegible]

CCANNAGATTNNTTGNAAACGNNNGTAGGCTTCTTTGTAGATTTATTGAAAAATGTTTCST
AATTCTACAAAGTTTGGCCCTGCTTCCATAAAAGAGTGAANTCANTTTGAATCGACTGG
TGGATAATTNTTCCATTTTTCTCAGGCAATTTNGAGTTACTCCAATAAAATTCAAATAT
GGBCCAGAGGAAATCATCTTTCAGATGGGCAGTGAATTGGCCAGTCAGCAGGAGAAAC
TGTTTATGCCTTGTTTGGTACATTGTGSAAAAACACACTTTAATAAATACGCANTCATG
CTTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT
CCATTGSGGAATAATTCCATGGTTCCGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG
ATCAANGGAGTGACAGTCAGTCCTGGGTGGCAAAAATGTCCCATTTTTTAAGTACCA
AGCAAAGGTTCTTCTTCAAGGGTTNCTAGGGCC

HC2A -----
 KIAA ASGNLEKNAHFSAIYRIIDENKLSNDCMLKLLADPHKKPEKMAKLPVILGNLDITIDNVSSD
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----
 KIAA FPNYVNSSY:PTKQFETCSKTPITFEVEEFVPCIPKHTQPYTYTNHLYVYPKYLYDSQ
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----VLHHHQNPFFYDEIK
 KIAA KSFARARNIAICIEFKDSDEEDSQPLFCIYGRPGGPVETRSAFAAVLHHHQNPFFYDEIK
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A IELPTQLHEKHHLLLTFFHVSCDNSSFGSTKKRDVVETQVGYSWLPLLADGRVVTSEQHI
 KIAA IELPTQLHEKHHLLLTFFHVSCDNSSFGSTKKRDVVETQVGYSWLPLLADGRVVTSEQHI
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A PVSANLPSGYLGQCGLGMGRHYGPEIFWVDGGKPLLKISTHLVSTVYTQDQHLHNEFFQYC
 KIAA PVSANLPSGYLGQCGLGMGRHYGPEIFWVDGGKPLLKISTHLVSTVYTQDQHLHNEFFQYC
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----GCTAESTVVISLINCARY
 HC5 -----

HC2A .PIETPAALRNHIVPEIKHAMPCHYMIAPIIILNLEPRLT-RATPEVAIVVTRV
 KIAA .PIETPAALRNHIVPEIKHAMPCHYMIAPIIILNLEPRLT-RATPEVAIVVTRV
 rat -----
 HC4 -----MEIQVLIFFLSVILMQLFVVLNMIHEDDVPISCPVV
 HC1 -----MSFLPIILNQLEKVLV-QNEEDEIITTVTRV
 HC3 NEDFALTNENHLLTPETPHLEPRLTQKRIEENQWNTSGPFAAPNCCNDPQAGC
 HC5 -----

FIG. 4B (1 of 5)

HC2A ITHVVAICHEEGLESHLRNYKYAYKAEPYVASEYKTWHEELTFSMTTILKPSADFLTSN
 KIAA ITHVVAQCCHEEGLESHLRNYKYAYKAEPYVASEYKTWHEELTFSMTTILKPSADFLTSN
 rat
 HC4 LPHIVSKCHFEGLISYLLSPFVYSIFREGFPNAPQAPLIHETLATMTIALPQSAFLAIN
 HC1 LPHIVAKCHEEQLDRSVQSYIKFNFKTR---ACKRRPVHEDLAKNVTGLLK-SNDSPTVK
 HC3 TQAMDPLONPMSSHTETSSPLQTLGRLP---TKKLCHHEELALQWVVCSG--SVK---E
 HC5

Cadherin

Cleavage

HC2A KLLRYSWFFFDVLIIPMAQHLIENSKVELLNNQRFPAVYHHAABTWNNMLMPHICQKFGD
 KIAA KLLRYSWFFFDVLIIPMAQHLIENSKVELLNNQRFPAVYHHAABTWNNMLMPHICQKFRD
 rat
 HC4 KLLRYSWFFFEIIPMAQHTYLEENKIKLNGQRFPPKAYHHAHSLFLAIT-TVHSQYAE
 HC1 KLLRYSWFFFEIIPMAQHLIDTNEIQLEAPQRFPEVQNELDNLMVMSLSDHFWKYKD
 HC3 SALQQAFFFFELMFAHVVHHLVFNDELEAPKSKFPPEFEMDDAALVSTIASDITSRVQK
 HC5

HC2A NPEAKHIANHSLAVEICRCFTIMDIQGVFVQIN---NYS---GFAPGDIKLEFHKFHEFL
 KIAA NPEAKHIANHSLAVEICRCFTIMDIQGVFVQIN---NYS---GFAPGDPIKLEFHKFHEFL
 rat
 HC4 IPKESRNVNYSLASFLICCLTIMDIQGVFVQIN---DYS---GFSPIPIVLANEFHEFL
 HC1 ALEETRIACHSVAKFLICRCFTIMDIQGVFVQIN---NYS---MFSSGDLICLQNFDFEL
 HC3 DTEMVEILNTSLAPFICDLISVMDQGVFVQIKSCYEQVSSKLYSLNPFVLMGLDDEL
 HC5

HC2A RVVCNHHHYIPLNLEM-----PFGGRIQR-----VQDLQL---DYALTDEF
 KIAA RVVCNHHHYIPLNLEM-----PFGGRIQR-----VQDLQL---DYALTDEF
 rat
 HC4 QTICNHHHYIPLNLEM-----AFAPFKLQR-----VQDSNL---EYGLSDEY
 HC1 QEVCQHHHFIPLCLPISANIPDPLTPSES-----CQELHASIMPEFVVTNEF
 HC3 RIICSHHHYVTLNLCIILLTPASEPQVSSATQSSHFSTNVQDQFIANFELM--VPE
 HC5 -----KADTAITSPEPSIS---SQNSLSCSSFDQDQFIANFDTCSRVP

Cadherin

EC motif

HC2A CRNHFLVGLLLREYGTALQEFFE---VRLIAISVLEKLLIFHSFDDRYASRSHQARIAT
 KIAA CRNHFLVGLLLREYGTALQEFFE---VRLIAISVLEKLLIFHSFDDRYASRSHQARIAT
 rat
 HC4 CKHHFLVGLLLRETSIALQDNYE---IRYTAISVLEKLLIKHAEDTRYQENQAKIAQ
 HC1 CEFHFLVGLLLREYGTALQEFFE---VERIALAILEKLLMAHGFDDRYAFEPQQAQIAS
 HC3 ELYHYAGIATRLAYILLIFAPGIQLHFFVIMINRMLLCHHSTFRYDQSHAPVAN
 HC5 QUTP-SIGIKETFAALCARYPGIDEMVPAWALHLILSPHLDPEGVYPPPEVKAIA

HC2A LYLLPFLNLENTLPIVLEKLLIFHNAFETVRIEUALHANNVNLIFKRTINLH
 KIAA LYLLPFLNLENTLPIVLEKLLIFHNAFETVRIEUALHANNVNLIFKRTINLH
 rat
 HC4 LYLLPFLNLENTLPIVLEKLLIFHNAFETVRIEUALHANNVNLIFKRTINLH
 HC1 LYLLPFLNLENTLPIVLEKLLIFHNAFETVRIEUALHANNVNLIFKRTINLH
 HC3 LYLLPFLNLENTLPIVLEKLLIFHNAFETVRIEUALHANNVNLIFKRTINLH
 HC5 LYLLPFLNLENTLPIVLEKLLIFHNAFETVRIEUALHANNVNLIFKRTINLH

2.1

[illegible]

FIG. 4B (3 of 5)

HC2A ATACQKREHENDPEMLVLLQVSLAKSYASTPELRITWLDQSNARINHYKNGDLEEAAMCYVHV
 KIAA ATACQKREHENDPEMLVLLQVSLAKSYASTPELRITWLDQSNARINHYKNGDLEEAAMCYVHV
 rat ATACQKREHENDPEMLVLLQVSLAKSYASTPELRITWLDQSNARINHYKNGDLEEAAMCYVHV
 HC4 ATACQKREHENDPEMLVLLQVSLAKSYASTPELRITWLDQSNARINHYKNGDLEEAAMCYVHV
 HC1 ATACQKREHENDPEMLVLLQVSLAKSYASTPELRITWLDQSNARINHYKNGDLEEAAMCYVHV
 HC3 ITVEMREHEDQDPENLLDLMVRIAKSYQTSFDLFLTLQNMAGHSESRSHHAAQAQDLVHS
 HC5 ITVEMREHEDQDPENLLDLMVRIAKSYQTSFDLFLTLQNMAGHSESRSHHAAQAQDLVHS

CH3

HC2A TALLVARYITFEFGV-----VQWHPPILPASHACLRKSEFGVFFGQCTAFKVTIPN
 KIAA TALLVARYITFEFGV-----VQWHPPILPASHACLRKSEFGVFFGQCTAFKVTIPN
 rat TALLVARYITFEFGV-----LALQHPPIFPFISHTSCQKRSFGVFFGQCTAFKVTIPN
 HC4 TALLVARYITFEFGV-----LALQHPPIFPFISHTSCQKRSFGVFFGQCTAFKVTIPN
 HC1 AALLVARYITFEFGV-----TASLLSHHTHPCSENILLTTPSCGSMFSHMKAPAFKVTIPN
 HC3 AALLVARYITFEFGV-----TASLLSHHTHPCSENILLTTPSCGSMFSHMKAPAFKVTIPN
 HC5 AALLVARYITFEFGV-----TASLLSHHTHPCSENILLTTPSCGSMFSHMKAPAFKVTIPN

ITAM

HC2A IDEBASIMEDAGMQD-----VHFNHIVIMELLEQCADGLWFAHFEIADITYELLII
 KIAA IDEBASIMEDAGMQD-----VHFNHIVIMELLEQCADGLWFAHFEIADITYELLII
 rat IDEBASIMEDAGMQD-----VHFNHIVIMELLEQCADGLWFAHFEIADITYELLII
 HC4 IDEBASIMEDAGMQD-----VHFNHIVIMELLEQCADGLWFAHFEIADITYELLII
 HC1 IDEBASIMEDAGMQD-----VHFNHIVIMELLEQCADGLWFAHFEIADITYELLII
 HC3 IDEBASIMEDAGMQD-----VHFNHIVIMELLEQCADGLWFAHFEIADITYELLII
 HC5 IDEBASIMEDAGMQD-----VHFNHIVIMELLEQCADGLWFAHFEIADITYELLII

ITAM ITAM

HC2A SEKRDEFLANLYDTLHPPSYVTEVNHIGERLLITVERVAFPPQAAQVGFDTGCTWAE
 KIAA SEKRDEFLANLYDTLHPPSYVTEVNHIGERLLITVERVAFPPQAAQVGFDTGCTWAE
 rat SEKRDEFLANLYDTLHPPSYVTEVNHIGERLLITVERVAFPPQAAQVGFDTGCTWAE
 HC4 SEKRDEFLANLYDTLHPPSYVTEVNHIGERLLITVERVAFPPQAAQVGFDTGCTWAE
 HC1 SEKRDEFLANLYDTLHPPSYVTEVNHIGERLLITVERVAFPPQAAQVGFDTGCTWAE
 HC3 SEKRDEFLANLYDTLHPPSYVTEVNHIGERLLITVERVAFPPQAAQVGFDTGCTWAE
 HC5 SEKRDEFLANLYDTLHPPSYVTEVNHIGERLLITVERVAFPPQAAQVGFDTGCTWAE

ITAM

HC2A -FFEDEDGPEIITHEPKLTPLEISQRIILISDRPGSENVENIQDGGINPFIQDSIFA
 KIAA -FFEDEDGPEIITHEPKLTPLEISQRIILISDRPGSENVENIQDGGINPFIQDSIFA
 rat -FFEDEDGPEIITHEPKLTPLEISQRIILISDRPGSENVENIQDGGINPFIQDSIFA
 HC4 -FFEDEDGPEIITHEPKLTPLEISQRIILISDRPGSENVENIQDGGINPFIQDSIFA
 HC1 -FFEDEDGPEIITHEPKLTPLEISQRIILISDRPGSENVENIQDGGINPFIQDSIFA
 HC3 -FFEDEDGPEIITHEPKLTPLEISQRIILISDRPGSENVENIQDGGINPFIQDSIFA
 HC5 -FFEDEDGPEIITHEPKLTPLEISQRIILISDRPGSENVENIQDGGINPFIQDSIFA

4.1

ITAM

HC2A LITVTHVTFEPIEHLVHYEPEPCHIIIFPMFHTITVVEIDVVEELVHIIIAA
 KIAA LITVTHVTFEPIEHLVHYEPEPCHIIIFPMFHTITVVEIDVVEELVHIIIAA
 rat LITVTHVTFEPIEHLVHYEPEPCHIIIFPMFHTITVVEIDVVEELVHIIIAA
 HC4 LITVTHVTFEPIEHLVHYEPEPCHIIIFPMFHTITVVEIDVVEELVHIIIAA
 HC1 LITVTHVTFEPIEHLVHYEPEPCHIIIFPMFHTITVVEIDVVEELVHIIIAA
 HC3 LITVTHVTFEPIEHLVHYEPEPCHIIIFPMFHTITVVEIDVVEELVHIIIAA
 HC5 LITVTHVTFEPIEHLVHYEPEPCHIIIFPMFHTITVVEIDVVEELVHIIIAA

FIG. 4B (4 of 5)

Coiled-Coil 1

HC2A	INCFPYVKKRIPVNYQHHTLNHIEVAIDEMSHVVELPQLQSSAEVDMIRLQLLQGGV
KIAA	INCFPYVKKRIPVNYQHHTLNHIEVAIDEMSHVVELPQLQSSAEVDMIRLQLLQGGV
rat	INCFPYVKKRIPVNYQHHTLNHIEVAIDEMSHVVELPQLQSSAEVDMIRLQLLQGGV
HC4	SNRPFYVKKRIPVNYQHHTLNHIEVAIDEMSHVVELPQLQSSAEVDMIRLQLLQGGV
HC1	HLFPFYVKKRIPVNYQHHTLNHIEVAIDEMSHVVELPQLQSSAEVDMIRLQLLQGGV
HC3	HAFPYVKKRIPVNYQHHTLNHIEVAIDEMSHVVELPQLQSSAEVDMIRLQLLQGGV
HC5	MEAFPYVKKRIPVNYQHHTLNHIEVAIDEMSHVVELPQLQSSAEVDMIRLQLLQGGV

Coiled-Coil 2

HC2A	VMQVNAGILAYAFALDDTNTKYPDNKVKLIIEVFRQFVEACGGALAVNERLIEIQTH
KIAA	VMQVNAGILAYAFALDDTNTKYPDNKVKLIIEVFRQFVEACGGALAVNERLIEIQTH
rat	VMQVNAGILAYAFALDDTNTKYPDNKVKLIIEVFRQFVEACGGALAVNERLIEIQTH
HC4	VMQVNAGILAYAFALDDTNTKYPDNKVKLIIEVFRQFVEACGGALAVNERLIEIQTH
HC1	VMQVNAGILAYAFALDDTNTKYPDNKVKLIIEVFRQFVEACGGALAVNERLIEIQTH
HC3	VMQVNAGILAYAFALDDTNTKYPDNKVKLIIEVFRQFVEACGGALAVNERLIEIQTH
HC5	VMQVNAGILAYAFALDDTNTKYPDNKVKLIIEVFRQFVEACGGALAVNERLIEIQTH

Coiled-Coil 3

HC2A	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
KIAA	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
rat	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC4	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC1	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC3	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC5	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS

Coiled-Coil 4

HC2A	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
KIAA	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
rat	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC4	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC1	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC3	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC5	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS

Coiled-Coil 5

HC2A	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
KIAA	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
rat	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC4	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC1	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC3	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC5	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS

Coiled-Coil 6

HC2A	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
KIAA	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
rat	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC4	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC1	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC3	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS
HC5	QDEMFANFEMAHELSEIMHEGICPLEKETS-VLEH LHFNAISGTFSTIMVGMTS

FIG. 4B (5 of 5)

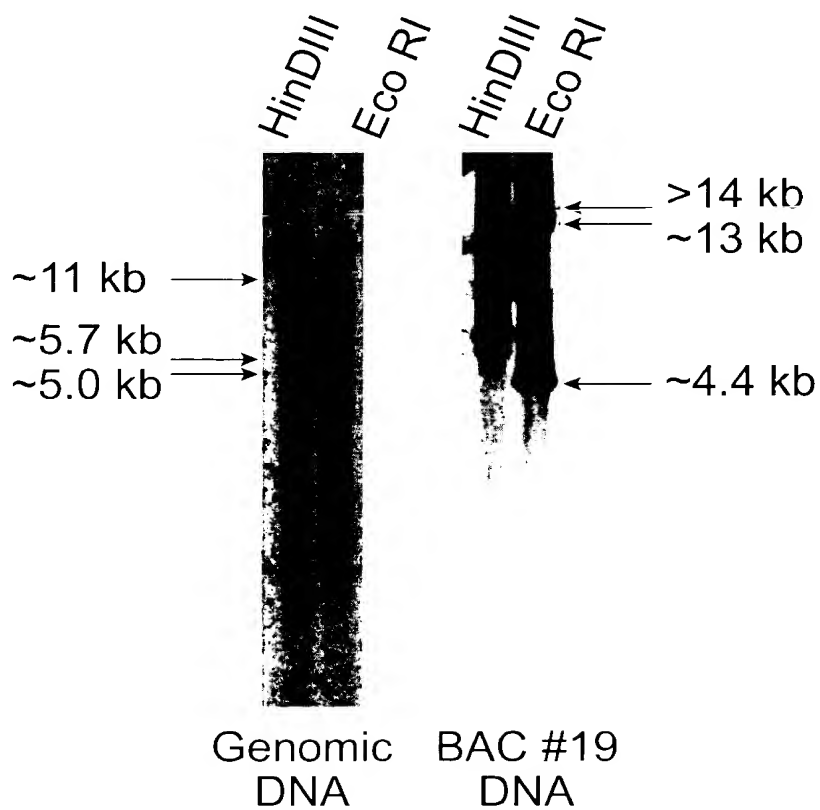


FIG. 5

-111

CGGTAACCGGCGATTTTGTCTGCTGTAACAATTTAGCGCGCGTGTAAGTGTGAATGTTTCAAAGCGCTCAGTTTATGACC
CTGTGGAAGTAATGGAGCTTTGAAGGACTTCTG -1

1/1	31/11
ATG ACA GAG CTG AAC AGC CTG GAT GTG CAG	CTT GCG CAG GAG CTG GGG GAC TTC ACT GAT
Met Thr His Leu Asn Ser Leu Asp Val Gln	Leu Ala Gln Gln Leu Gly Asp Phe Thr Asp
41/11	61/11
GAG GAG TTG AAC CTG GTG TTC ACG CCA AAG	GAA TGT AGG ACT TTG CAG CCC TGT TTG CCG
asp asp leu asp val val phe thr pro lys	glu cys arg thr leu gln pro ser leu pro
121/11	151/11
GAG GAA GCG GTT GAA CTG GAC CCT CAT GTC	AGG GAG TGT GTT CAG ACC TAC ATC CGT GAG
glu glu gly val glu leu asp pro his val	arg asp cys val gln thr tyr ile arg glu
181/11	211/11
TGG CTA ATG CTG AAC CGG AAA AAC TAA GGA	AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT
trp leu ile val asn arg lys asn gln gly	ser pro glu ile cys gly phe lys lys thr
241/11	271/11
GGA TCT CGA AAA GAT TTT CAC AAG AGC CTT	CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG
gly ser arg lys asp phe his lys thr leu	pro lys gln thr phe glu ser glu thr leu
301/11	331/11
GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC	CCC CGG CAC TTA AAC GTG CTG TGC GAC GTG
glu cys ser glu pro ala ala gln ala gly	pro arg his leu asn val leu cys asp val
361/11	391/11
TCT GGG AAA GGC CCC GTC ACT GGC TGT GAC	TTT GAG CTC CGC AGC CTG CAG CCG GAC AAG
ser gly lys gly pro val thr ala cys asp	phe asp leu arg ser leu gln pro asp lys
421/11	451/11
CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT	CCC GAG GAC TTT GAG AAG CAG AAC GAG GAG
arg leu glu asn leu leu gln gln val ser	ala glu asp phe glu lys gln asn glu glu
481/11	511/11
GCC CGG AGC ACC AAC AGG CAG GCG GAG CTC	TTT GCG CTT TAC CCA TCA GTG GAC GAG GAG
ala arg arg thr asn arg gln ala glu leu	phe ala leu tyr pro ser val asp glu glu
541/11	571/11
GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA	TGT CCG AAG GAA CAC CTG GGC AAC AGA ATA
asp ala val glu ile arg pro val pro glu	cys pro lys glu his leu gly asn arg ile
601/11	631/11
TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG	ATT GAA ATT GAG CCC CTG TTT GCG AGC ATT
leu val lys leu leu thr leu lys phe glu	ile glu ile glu pro leu phe ala ser ile
661/11	691/11
GCG CTC TAC CAT GTT AAA CAA AGC AAA AAG	ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC
ala leu tyr asp val lys glu arg lys lys	ile ser glu asn phe his cys asp leu asn
721/11	751/11
TCT CAG CAG TTT AAA GGA TTT TTT GGA GTT	CAC ACC CTT TTA GTG TTT GAA TTA AGT CAG
ser ser his thr thr gly phe leu arg gln	his thr pro ser val ala ala ser ser ile
781/11	811/11
TTG AAG TTT TTA GGT TTT TTA GGT ATT TAT	TTT TTT TCA GAT ATT TAT TTT TTA TTT AAG
leu arg thr thr thr gln phe leu thr thr	ser ser asp ile tyr leu val val lys
841/11	871/11
ATT GAA AAA ATC CTG CAG CAG GGA GAT ATT	GGA GAG TGT GCA GAG CCC TAC ACG GTT ATC
ile glu lys val leu gln gln gly asp ile	gly asp cys ala glu pro tyr thr val ile
901/11	931/11
AAA GAA AAT GAT GGT GGA AAG AGT AAA GAA	AAG ATT GAA AAA TTA AAA CTC TTA GCT GAA
lys glu asp asp gly gln lys ser lys ala	lys ile gln lys leu lys leu gln ala ile
961/11	991/11
GGT TTT GGT GGT GGT GGT GGT GGT GGT GGT	GGT GGT GGT GGT GGT GGT GGT GGT GGT
gly thr gly thr gly thr gly thr gly thr	gly thr gly thr gly thr gly thr gly thr

FIG. 6A (1 of 6)

3331/1111	GCT	ATC	AGT	GAA	ATT	CAG	AGC	CTG	CTA	AGT	TAT	CAC	GAC	CTG	GAT	CCA	CGC	TGT	CTC	AAA
3331/1111	ala	val	ser	ala	ile	his	ser	leu	leu	ser	ser	his	asp	leu	asp	pro	arg	cys	val	lys
3331/1111	GAA	GAG	GTC	AAG	CTC	AAA	ATC	GCC	GTC	TTT	TAC	CTA	GCT	TTA	GTT	GGC	ATC	ATT	TTG	GAT
3331/1111	gln	gln	val	lys	val	lys	ile	ala	ala	leu	tyr	leu	pro	leu	val	gly	ile	ile	leu	asp
3431/1141	GCT	TTG	CCA	CAG	CTC	TGT	GAC	TTT	ACA	GTT	GTA	GAT	ACT	CGC	AGA	TAC	CGC	ACC	AGT	GGC
3431/1141	ala	leu	pro	gln	leu	cys	asp	phe	thr	val	ala	asp	thr	arg	arg	tyr	arg	thr	ser	gly
3431/1141	TGG	GAT	GAA	SAA	CAA	SAA	GSA	GCC	GCT	GCC	ATT	AAC	CAG	AAT	STG	SCT	CTG	GCC	ATA	SCA
3431/1141	ser	asp	gln	gln	gln	gln	gln	gln	ala	gly	ala	ile	asn	gln	asn	val	ala	leu	ala	ala
3541/1161	GGG	AAT	AAT	TTC	AAT	TTG	AAA	ACA	AGT	GGA	ATA	GTG	CTG	TCT	TCC	TTG	CCC	TAT	AAG	CAG
3541/1161	gly	asn	asn	phe	asn	leu	lys	thr	ser	gly	ile	val	leu	ser	ser	leu	pro	tyr	lys	gln
3601/1201	TAC	AAC	ATC	CTG	AAC	GGC	GAC	ACT	ACT	CGC	AAC	CTC	ATG	ATC	TGC	TTT	CTC	TGG	ATC	ATG
3601/1201	tyr	asn	met	leu	asn	ala	asp	thr	thr	arg	asn	leu	met	ile	cys	phe	leu	trp	ile	met
3601/1201	AAA	AAT	GCT	GAT	CAG	AGC	CTC	ATT	AGG	AAG	TGG	ATT	GCT	GAC	CTG	CCA	TCA	ACG	CAG	CTC
3601/1201	lys	asn	ala	asp	gln	ser	leu	ile	arg	lys	trp	ile	ala	asp	leu	pro	ser	thr	gln	leu
3721/1241	AAC	AGG	ATT	TTA	GAT	CTA	CTT	TTC	ATC	TGT	GGT	CTA	TGT	TTT	GAG	TAT	AAG	CGA	AAA	CAG
3721/1241	asn	arg	ile	leu	asp	leu	leu	phe	ile	cys	val	leu	cys	phe	gln	tyr	lys	gly	lys	gln
3841/1281	AGT	TCT	GAC	AAA	GTC	AGT	ACC	CAA	GTC	CTG	CAG	AAG	TCA	AGG	GAT	CTC	AAG	CCC	CGG	CTG
3841/1281	ser	ser	asp	lys	val	ser	thr	gln	val	leu	gln	lys	ser	arg	asp	val	lys	ala	arg	leu
3901/1301	GAA	GAG	GCT	TTG	CTG	CGT	GGG	GAA	GGG	GCC	AGA	GGG	GAG	ATG	ATG	CGC	CGC	CGG	GCT	CCA
3901/1301	gln	gln	ala	leu	leu	arg	gly	gln	gly	ala	arg	gln	glu	met	met	arg	arg	arg	ala	pro
3961/1321	GGC	AAC	SAC	CGA	TTT	CCA	GGC	CTA	AAT	GAA	AAT	TTG	AGA	TGG	AAG	AAA	GAG	CAG	ACA	CAT
3961/1321	gly	asn	asp	arg	phe	pro	gly	leu	asn	gln	asn	leu	arg	trp	lys	lys	gln	gln	thr	his
4021/1341	TGG	GGG	CAA	GCT	AAT	GAG	AAG	CTA	GAT	AAA	ACA	AAG	GCC	GAG	TTA	GAT	CAA	SAA	GCC	TTG
4021/1341	trp	arg	gln	ala	asn	gln	lys	leu	asp	lys	thr	lys	ala	gln	leu	asp	gln	gln	ala	leu
4081/1361	ATC	AGT	GGC	AAT	CTG	GCT	ACA	GAA	GCA	CAT	TTA	ATC	ATC	CTG	GAT	ATG	CAG	SAA	AAC	ATT
4081/1361	ile	ser	gly	asn	leu	ala	thr	gln	ala	his	leu	ile	ile	leu	asp	met	gln	gln	asn	ile
4141/1381	ATC	CAG	CGC	AGC	TGC	GCT	CTG	GAC	TGT	AAA	GAG	AGC	CTG	CTG	GGA	GGT	GTT	CTG	AGG	GTG
4141/1381	ile	ala	ala	ser	ser	ala	leu	asp	tyr	lys	asp	ser	leu	leu	gly	gly	val	leu	arg	val
420																				

5611/1871
 ATT GAA GCT GCT ATT GAA GAG ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAG
 ile glu val ala ile glu asp met lys lys lys thr leu gln leu ala val ala ile asn
 5641/1891
 CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
 gln glu pro pro asp ala lys met leu gln met val leu gln gly ser val gly ala thr
 5701/1901
 GTA AAT CAG GGA CCA CTG GAA GTA GGC CAA GTG CTT ITG GCT GAA ATT CCT GCT GAT CCA
 val asn glu gly pro leu glu val ala gln val phe leu ala ala ile pro ala asp pro
 5761/1921
 AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG TTA CGC TTT AAG GAA TTC ATC ATG AGA TGT
 lys leu tyr arg his his asn lys leu arg leu cys phe lys gln phe ile met arg cys
 5821/1941
 GGT GAA GCT GTA GAG AAA AAC AAG CGT CTT ATC ACG GCA GAG CAG AGG GAA TAT CAG CAG
 gly glu ala val glu lys asn lys arg leu ile thr ala asp gln arg glu tyr gln gln
 5881/1961
 GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTT AGG CCA ATG ATC GAG CGG AAA
 glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys
 5941/1981
 ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
 ile pro glu leu tyr lys pro ile phe arg val glu ser gln lys arg asp ser phe his
 6001/2001
 AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA
 arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

GAAAAGCCATCTTCATTGCTGGAGACTGTGGCCCTGSAACCTGSGAGAAGGACTTGCTGGTACTTAAAAAATGGGACATT
 TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCGAGGAACCATGGAATTATT
 CCGAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGCTGGGCGGATGGAGGATGGGTACTCAGGATGACTGGGTAT
 TTATTAAGTGTGTTTTTCCACAATGTACCAACAAGGATTAAGGAGCTTTCTCTGCTGACTGGCCAAATCACTGCCCATC
 TGAGAGATGATTTCCCTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTTGCTGAGGAAAAATGGAAAAATTATCC
 ACCAGTCCGATTCAAACCTGAATTTCACTCTTTATAGGAAAGCAGGGCAAACTTTGAGGAGTACGAAACATTTTCAATAAAT
 CTACAAAGGGAAGCCTTACTACAATTTCAAAAAATCATCATGTTTGGAAATTTGGGAGGAGATTATTTGTGAACCTTGTTAC
 CTTTTTGGTAATGGTGGACTAATTTGCTGTATAGTTATTTTTTGTATTTATTATTACGTTACATTAATTTAACATGCATTTA
 TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACATGGTACTTGGAGCAGTCAGCCAAAAATTCACAGATACTGCTTT
 CACTTAAATGSAACAATTTCTCCGATAATGCTTTGCTTTTTTTCTTATGTCACTCTTTGTTACTATCTATTTTCTCCCTC
 TCCGGGAACCAAGTTTCTTTTTATAAAGCAATAATATCTGTGTTTTCATTTGAGAACATTGTGCTGTCTCTCAGGCATATGT
 ATATCAGCTACAAAAATATATTCAACTTTTACTTCTTTTACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
 AGAATTAATTTATATATTTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAAA
 AAAAAAAAAAAAACTCG

FIG. 6A (6 of 6)

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1737	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

FIG. 6B

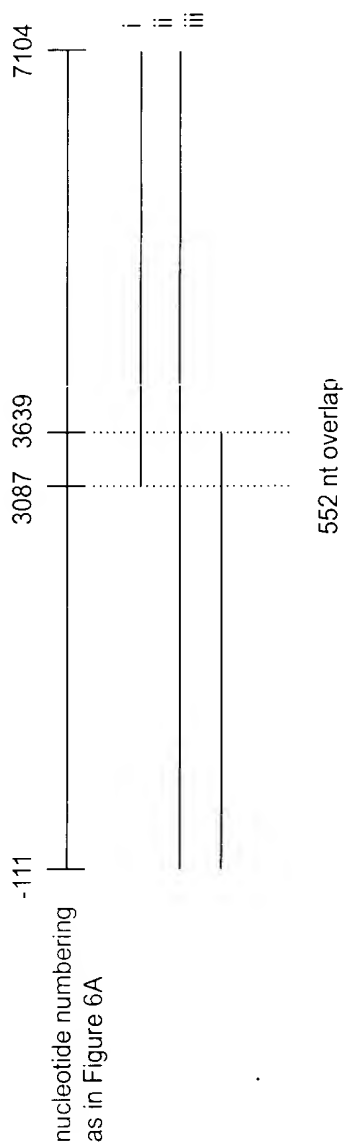


FIG. 6C

1st partial exon (nucleotides 3793 to 3950)
CCAGCTGTCAAGCAAGCTCAGTAACCTTCCAAACGCTCATTTCATGAGGCTAG
AGTTCCTGAGAAATCCTCTGTAGCCATGAGATTAACCTCAATCTGAACCTTTTT
TTTATGAATGTGATACCTCTCAACATCTCTTGTCTTCCATATCTTCCCA
GTAAATAAAGAATTATTTAATAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5809 to 5945)
GCTCAIAAAATGGCTCCTTACGTTTCGTAGAACTCAAGCTCCTGCTCCAGCT
TCCAGGACCCAGAAAGATCGCCAGCATGTTCSATCTGACTTCCGAGTACCGCCA
GCAGTACTTCTCACCAGGCTCTCTTTTCAAGAACTGGCTGCTGCCCCGGATG
CCGAAAGGGAAGGGTATGTTTCTGGCATTTAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)
CATAAGCTCTTGATTCCTGTCTTGTCGCAACAATCAGCAAAATACAAAGG
AAAGCTGTCAGTGCATTCACAGGCTCTTAAGTTCTCAGCAGCTGGACCCCA
CTGTGTCAAAATCAGAGGTCAGAGTCAAAATGGCCGCCCTTACCTACCTTTA
GTGGCATCATTTTGGATCTTTTGGCACAGCTCTGTGACCTTACAGGTAATGG
CCCTTCTGTTTCTTCTTGGATG

4th exon (nucleotides 16948 to 17087)
TGTTTCACTTCAATCAAAAAGATGTTTTCATTGCACTTGCACTACTGCA
GATACCGGACCCAGTGGCTCGGATGAAGAAACAAGAAGGAGCCGGTGCATTA
ACCAGAAATGTGGCTCTGGCCATAGCAGGGAATAATTTCATTTGAAAAACAAG
TGGAATAGTGTCTGCTTCTCTTCTATGTTGGTGCACATGTGTCTGGTTGATTTT
TCAT

5th exon (nucleotides 19381 to 19463)
TGBCCTCCATCCCCCAATCTGCTTCCCTTCAGCCCTATAAGCAATACAACATG
CTGAAAGCGGACACTACTGGCAACCTCATGATCTGCTTCTCTGATCATGAA
AAATCTGATCAGAGCTCATTAAGAACTGGATTCTGACCTGCCATCAAGG
CAGCTAACAGGATTTACATCTATTTTCATCTGTGTCTTATGTTTGAATAT
AAGGTAAGTCTGAACTGGCACTTTTATACCAGC

6th exon (nucleotides 19829 to 19958)
CACCAAAAGGATATGTCCTCCTACCTCTCTCTTGTCCAGGGAACAAGATTCT
GACAAAATCACTACCCAAGTCTGCAAGATCAAGGGATGTCAAGGCCCGG
CTGGAAGAGCTTTTGTCTGCGTGGGGAAGGAGGACAGAGGGGAGATGATCGGC
CCCGGGGCTCCAGGTGTGTGGACTGGGCTTCTCTGCTCTCTGCAAGC

14th exon (nucleotides 38125 to 38268)

CTGTTCTCCAGGCTTATAGTGTGTCTCTTTCAATAATTTCTTCCAATGTGCT
GGAGGAGTCTGTGGTCTCTGAGGACACCCCTGTACCTGACGAGGATGGGGTGTG
CCCAAGCCAGTACTTCCACCGAGAGTGGGCTGGTAGGGCTCCTGGAGCAGG
CCGCGAGGCTCTTCAGCACGGTCAGTGCTCAGAGGGCATCCCCGGGGCTGGC
C

15th exon (nucleotides 40166 to 40297)

AATTCTCTCTGATGCTCTTCTCCTCTCTCCAAGGGAGGCTTATATGAGACAGT
TAATTAAGTCTACAAGGTGTGTCACTCCCACTAGTAAGCGCATCGAGAAATTC
CGGAAGTTGACACTCACTCACAACAAGTTGCAGAGAGGCTTCGACAGCATCG
TTAACAAGGTAGCCGGGGAGCTTGGCTGGCAGGTCCTGTGTAC

16th exon (nucleotides 40755 to 40889)

TAAGGAGAGCCTTTTTATATTTTGTTCCTCAGGATCATAAAGAGAATGTTTGGAA
CCCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTGTGATGAACAG
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG
ACTAGAGGTAACAAAAGTGATTCTGTGCGCTGACTTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)

AACCTTTATAAACTGTTGGTCTTCTTACCTAGGCATTTTATGSTCAATGTTTT
GCTGCAAGAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA
AGTTGGATCCTAACCAAGGTATACAAAATTTACAAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)

CTTCTCTCCTCTGTGCCCTTTTCCCTTTAGGCTTACATACAGATCACTTTTGTG
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACITTGAGAAGA
ATTTCACCTCTCGGAGGTTATGTATACCCAGCCCGTTCAACCTGGAGGGG
GCGGCTCTGGGGGAGAGCTGCAATGAGCACTACAGAAGGAACACAGTCCCTGAC
TACTATGTACGGCTTCCCTTACATCAAGACTAGGATGAGCGTCATCCAGAAG
GAGGAGCTAATCCACCAAGGATAGGCACTCACTGATCAGT

19th exon (nucleotides 46664 to 46807)

ACAGTGAATTCCTATGTCTTADGTCTCATGTCTAGTTTGTTTGATCCGATTCG
AGGTGCTATTGAAGACATGAAGAAGAAGACCCCTGCAGTTAGCAGTTGCCAT
TAACTAGGAGCCCGCTGATGCAAGATCTCTCAGATGCTGTGCTGCAAGGCTCTGT
GGGAGCTACTGTAAATCAGCTAAGCAAAACACAGGTGGCAGCTCCT

CTTGAATTTCACTAGG

FIG. 7A (3 of 4)

T C A T T T A T T T C T C C C A C A C T G A T A T T T T C A T C T C A G A T G T S S T G A A G C T G T A
A G A A A A A C A A G G T C T C A T C A C G G G A G A G A C C A G A G G G A A T A T C A G C A G G A A C
T C A A A A A G A A C T A T A A C A A G G T A A A A G A G A A A C C T C A G G C C A A T G A T G G A G C
G S A A A A T T C C G A A C T S T A C A A G S C A A T A T T C A G A G T T G A G A G T C A A A A G A G
T A A G A A T C A G G G C A G G G A G G C C C T C C T C C T G G G A T

OCTCCCTTCTTTTCTTAATTTGAGGGACTCCTCCACAGATCTAGTTTCAGGA
 AATGTGAAACCCAGTTTGTACAGGGCAGCTAAGAAAAACCATCTTTCATTGCT
 GAGACTGTGGGCTTGCAGAGCTGTGAGAGAGGACTTGTGTGCTACTTAAAAAAT
 GGGACAITTGGCACCACAGGACTGACTGTACACTCCCTGATCAGCCAGCACT
 TGGAGGCTTTGGGATCCCAAGAACCATGGAATTATTCCCAAAATGGACTCTGA
 CCAGATITTTGGCATACTGGGGGGTGGGGGGATGGAGGATGGGTACTCAGGG
 ATGACTGGGTATTTATTAAGTGTGTITTTCCACAATGTACCAAAACAAGGCAT
 AAGCAGCTTCTCCTGCTGACTGGGCAAGTCACTGCCCATCTGAGAGATGATTT
 CTGTGGCCCATATTTGAAATTTATTGGAGTAACATAAATTGCTCTGAGGAAAAAT
 GGAAAAAATTATCCACCAGTGGATTCAAACTGAATTTCACTCTTTATAGGAAG
 GCAGGGCAAACTTGTAGGAGTACGAAACATTTTTCAATAAAATCTACAAAAGGGA
 AGCCTTACACAAATTCAAAAATCATCATGGTTGGAAAAATTGGGAGGAGATT
 ATTTGTGAACCTGTGTACCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTAT
 TTTGTCTTATTTATTACTGTATCATTAATTTAACATGCATTTATAGAAGAAATAC
 ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA
 ATCAAGATACTGCTTTCCTTAAATGGAAACAATTCTCCGATAATGCTTTGC
 TTTTCTTTTATATGTCACTCTTGTGTAATATCTATTTTTCTCCTCTCTGGGACCAA
 GTTCTCTTTTATAAAGCAATAATATCTCTGTTTTTCATTTTCAGAACATTGTGCTG
 TCTGTACGATATGTATATCAGGTACAAAAATATATTCAACTTTGACTTCTTTTG
 ACAAAAGCACTTAGGAAAAGGAGGAACAAGACATTATTGTGAGAATTAAAT
 ATATATTTTTTAATATGACTGTGACCTTGACTGATAATAAGAGATGTAATAAGAA
 TTGCAAGCTAAAAAAAAAAAAAAAAAAAA

FIG. 7B (1 of 15)

FIG. 7B (12 of 15)

TGGGATAATGTTTGGTTTTTCTTTATATGTAATTTCTGTCTACTATCTATTTTTCTCTCTCTCTGGGAACCAAGTTTCTTTT
 TATAAAGCAATTAATATCTTGGTTTTTACTTCAGAAATCTGTCTGTCTGTCTAGGATATGTATATACAGCTACAAAATATAT
 TCAATTTTGGATCTTTTGGAAAAATTTAGGAAAAAGAGGAAACAAAGACATTTATTTGAGAAATTAATTTATATATTTT
 TAATATGATTTGAGCTTGAATATATTAATTAATTAAGAAATTCGAAGCTAAATGTTTTCTTTGGAACTGATGTTTT
 TCTTTTTTATTTGATGATGCTACTTCTCTGTAATTTTTTGAAGGCACTTCAGAGAGAAAGAGATGCAATCTCTGTCCT
 TCTATCAAAATTAAGACTATCCCAAGGTCGCACTTTCTCTCAATGTTTAACCTCTCTGAGTAAATCAAGGATGACTTAGTTGGG
 ATATTTTCAGAAATTTTTTGGTTATACCATCAGATATGATSAATTTATAATCTTGAAGAGTACTTAAAAATTAATTAATAA
 CTTCACAGCTTAAGTGGTAAATTTTTATTTTATAGGTATTTGGGGAAGAACTCTTTTAAAGATATACACCTAACTGCTT
 TTTAAAAATGACTACACATGACATACCTTTAAATTCATATGTATTTCCCTACTCTTTGGGAACACCTGGTTGAGACCAAGG
 TCAAAAAACCTGGTCCACCGCCCTCCAAATCTCTTCTGGTCTCTGAGGAAGATATATATCTTGGTATATAGGCCACAGTACA
 AAACAGACTACAAACACAGCCCATAGCATGTAATTTTTCTCTGACTAACTCAAGGATAGGTTCAACATATATGGTATTAGAT
 TGTGCTCTAAACAAATGAAGATTAGATGCTAAATATATAGTCTCTGAGCTTAACTCAAAATAGGCAATATAGGCTCTAGTA
 AGCTAGAAATTTCTGATTAAATATCTCTCTCTTTTATAGATACCTGTTCTCTCAATTTGGGTTTGGTTTTTACAGTCTCTTTT
 GTACACAGCTGATACATTTTGGTTTCACTGAGTGGAGGAACTGTTCACTGCTGCAATCTTACCTCTAGGCTGCAACAAA
 CACACAAAACATACCCCAATAAATATTTGTTCAATCACATAATGAATGAATGATGAGTAGGCTCTCTCTCTAGAGGTGCACT
 GCAATAAGAAATGTAATGCAAGCCCATATATTAATTTAAAAATTCAGAGGCTATATAAAAATAAATATAGGCCAAGT
 GGAGTGGCTCTACATGTAATACCACTCTTTTGGAGACCAAGGTCGGGCAGATCACTTGAAGCCAGGAGTTTGAAGCCAG
 CTGGGCAAAATGGCTAAACCCCATCTCTTAAACAAAAAGATATAAAAAATTAAGCAAGTGGGTTGGTAATGGCTCTGAGT
 CCGAGCTACTCGGGAGGCTAAGGTCGGAGGATGCTTGAAGCCAGAAAGTTTGAAGGCTGCACTGAGGCAATGATCTGCTGAC
 TGGCACTCTAGCTGGGTGACAGAGTGAAGCCCTGCTTCAAAAAATAATCAGCATATATAAAAAAGAAACAGGCAAAATTAAC
 TTTACTAGTATATTTAAACCAATATATATAAAATATTATTTCAATATGCTTCTCTATATAAAAAATATTTTACAGTCTTT
 TATTTCCATATTAAGTCTTTAAAAATCTGATGTTAGTCTTGTACTTACAGCACTGTTGCAATTAAGGATGGCCACATTTTA
 AGTGGACAGTACCCACAGGGGGCCACTGGCTACCATATGGGATAGTGGCAATCTAGAAAGTTTCAAGTTTTTCAACTGGA
 TGCTCTGATTTGTGGACTCAGAATACAGATAACCAAGAAGTGGGACTAGTGTCTGAAATGAAGATGACAGGGTATGAT
 TGAGAGCCCTCAGGCTTACCTAGGAGAGAAATTTGTGGGGTTGCAAGAAAGGATTTGTCATATGGCTCTAGCTGTT
 CACACTATTCTGGGGCAACTCCAGATCATTCTCAACTCCAGATAGTTAAAGTGGGGAAGCATGCTGCTGACTTTTAAAG
 TGATGGCACAATAAAGATATTGAACGTTGGTCTCTGATATATATTTCAAAATATGCAATTAAGAAAGAGGCTTTTAA
 GAATCCCTAAGAGTAAGCAAAATAGTATCTTTGTTTCTGAAATTAAGAGAAATTTGATATGCTATGATAGCCCTCTCTC
 ATTTTATTTGGAAAATCTTCTATGAAAGCTTATAGAGAAATTTCTGATTAGCTTCAAGCTCTCTCTCTCTCAGCAA
 GGTCAGGGTGCAGTTGCTCACTATCACATAAGAAATCTCATAAAATTAACATGAAATACTCTGCAAGATCTGATTGGGT
 TTGTCATGCCACACATTTGTTTAAATTCATATTTCTATATAAAGAGTCTTTCTATAGCAATAGATCTGTTTAAAAA
 ACAAAACAACAAACAAAATTTAGAGTTGTCATTGGTAATTTGGTTGCAAGTATGCTTTTAAAGATAGAGGCTTTTGT
 TTGCTTTGAATGTAATTTTTTTCTTTTTCTTTTTTATACGGAGTCTCACTCTGTTGGCTAGGCTGGAGTGCATTGGCAC
 CATCTCAGCTCACTGCAACCTCCACCTCCGTGGTTTAAGCAATTTCTCTGCTCAGGCTCTCTGAGTAGCTGGGATTACAG
 GCGTCCACCACCAGGCTGACTAATTTTTGTATTTTATAGTACAGATGGGGTTTTTACCATGTTGGCCAAAGCTGGTCTCAAA
 TCTCTGACTCAGGTGATCCACCTGCTCTGCTTCCAAAGTGGTG

FIG. 7B (15 of 15)


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hCLASP4 -----MFPMDISICTVIGRQETVC----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFACKIARKTVAAEVRVQISGQYSGSPQLLNLTNG 41
hCLASP1 -----MLLPYDDDFCTALRRQGVICS----- 23
hCLASP7 -----MAASERRAFAMKINRTVAAEVRVQVSRERBGSFHSRRCSSIL 43
hCLASP1 MSFRGKVFKEPSEFWKKRATVRRVIGEEFHRFSSQEKPLILEPLDVECTVIELEKTYEN 60
      . . . . .

hCLASP4 -----STVPRDAEKHAQSLHVRECIKTYSDWHVWTK 53
hCLASP5 -----DPT 19
hCLASP7 N-----LPHHTTVPLTHAVCPVLDLDYDITHPLAVDSGPHLDLCEP 85
hCLASP2 -----TVPAKAEERFAQSLFVTECIKTYSDWHVWTK 53
hCLASP7 S-----VPLTEVTEPLDVEDVLLSNPPDAEPGGLDLMVEPP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDITRTLYSTVPDAEKHAENILVREACHFYSQDWHVWTK 110
      . . . . .

hCLASP4 YEDYSGDFRMLPKCSLRPEKIPNHVFELDEDECEDED-----SSSLGNSQPGGVTKIG 105
hCLASP5 DDDIDVYVETPKFQRTLMFP-SLPEECVELEDPVT-----DCVQTYIEHW 63
hCLASP3 PDDIEVYSPFCRTHLY-AVPEE-SEMDPHV-----DCIFSYTLDAW 125
hCLASP2 YEDYSGDFRQLPNKVMELDHLVHVVEVDEEDVDED-----AASLGGCIGGCTHHS 107
hCLASP7 ADDLELLQLPECRTHI-GIPEK-ENLDACV-----AAVENILHFW 121
hCLASP1 YEQYSGDIRQLPRAFYKHELPSHSEFIDHEIDKDEDTTCHS SKGGGAGGCTGVFKIG 180
      . . . . .

hCLASP4 WLRFANVNSTIT--VTHVFFHRYFYLTQLDLSYILNSYFDEFNSKEK-GCIYLDW 161
hCLASP5 VNRFNQGSPEIC--GPHFTGKRDPHKT-LEHCTESESETLECSI PAAQA--GPHINTIC 118
hCLASP3 VIRKZYHLGTGF--NNITLDQHERQKG-LEHCTESEDEAHGMSYQDDQDDPFRSM 180
hCLASP2 WLKFGNMNSAIS--VTHSFHFFHFLIQGLDLSYINIFYDEFISKEK-GSIFLDW 164
hCLASP7 VHKRYQLSAAY--HPVTDTCQERQKG-LPHQA EQDASGDERSGPDSNDSEFGSG 179
hCLASP1 WLKFGNFNSTVNTVTVRSEHRYFYLTQLDLSYIMNFYDEFISKEK-GSIFLDW 239
      . . . . .

hCLASP4 DWVQCFMRRHAFELHMLDHYSHYLAATEQEENEELITLKFIIQINTDSIQEHFET 224
hCLASP5 DVSQGFQVTAQDFELHLOPHLENILQVSAEDFEKQNEEAPFTN-----EQAE 169
hCLASP3 DDTPRGSWACSI FDLHSLFDALLPNLLDPTNHEIDRQNDQDKSN-----RHAE 234
hCLASP2 GTVQNNVVRFFAFELHMQHSSYLLAADSEVENEHWITILNKILQLN-----FEAAMQEK 219
hCLASP7 EDTPRSSGASSIFELHMLAADLLPSLLERAAPDVDRRNETLRQH-----RPPA 230
hCLASP1 GTVQNNRLRYAFELHNDLTYFVLAATESDMDEWIHTLNRILQISPEGLQGRETEL 299
      . . . . .

hCLASP4 TAQDEBTSS----QRAENIMASLERSMHFELMKYGPETQLNKLSPGDERQWLF 278
hCLASP5 IFALYIYV-----EITVNHIFETETFFHLS-----N-----LIVVPLTHFEN 311
hCLASP3 SHAIHEDT-----EHEIDELTYEIHFEHP-----HLDVPLSLFEN 277
hCLASP7 ENATHEFI-----ELVLEHGLGLTYFELHVAEARIK-----LVEFINKLF 311
hCLASP2 LIDYTAH-----HLEHNEVRIETFRPH-----HLDVPLSLFEN 277
hCLASP1 TILHIDELQVTHVTHETESGFNNHAEPRVITETETVWTTNKHILFEL 278
      . . . . .

hCLASP4 VIELDPS----GIMDIFP-FEEKONRFLVNHOLTENILGQIGONAKGPETNVEP 334
hCLASP5 IEPLFAS----IALDVKERKYSFENFHODN: DQKGFLEAHTPSVAASSQARSASF 268
hCLASP7 LPHIFAS----LALDVKERKYSFENFYFDLNSGMSGLLEHVPFAITILAKSIF 333
hCLASP2 ALKILF-----LAFHEVT-FPEFPHILVKNILFENLITVAENREGETTVSEPV 333
hCLASP7 IELIFN-----IALDVKERKYSFENFYFDLNSGMSGLLEHVPFAITILAKSIF 333

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hCLASP4 NLALFVFNNTDFISALFHVILNFFSVREMLWSSSTQLASIGSP---KSSSPESYIHGTAR 393
 hCLASP5 TYPSSDVLVTVKIEKVLQSGD----IGDAAFPYTVKEIDG-----GHSHE-HIEKLAL 317
 hCLASP3 TPSSQDVLVTVKIEKVLQSGD----IGDAAFPYTVKEIDG-----TEN-E-LEKLAS 362
 hCLASP2 TSLSPDLVYNREISAEFFVNLNHFSSVPCMLATTSPALMIGN-----GDC-SVAKGLAE 381
 hCLASP7 TFFSFLVTVKIEKVLQSGD----IGDAAFPYTVKEIDG-----AAN-E-ALEKLAL 375
 hCLASP1 SVALYDAAKSKHISALEHVLNHAAYRQILLGASVALENGVDTITPRSHPEPHKGLPE 479
 * * * * *

hCLASP4 GNLRIYALGIFENWPPHIEFLVARIKVLQGNITHCANPIHNSDPVHTAQKURHTAQ 450
 hCLASP5 QAESDGLK-----LGRHMPFANAKISLGGFTVSTLERETDQDVSVMGR PWRHRTIA 572
 hCLASP3 QADQPCQR-----LGRHMPFANATHEMINIVISAGSLHROSTEVETSTGRKRLWHERR 437
 hCLASP2 AANQYPRGIGFSVACNPPDIFLVARIKVLQGNITHCANPYMKSSSDSSVAQKRLKNAQ 441
 hCLASP7 AANQPCQR-----LGRHMPFANATHEMINIVISAGQLDRSD----SFGREFPAWTDER 429
 hCLASP1 ENLXPPHJAVFSVINDHSHIVLAKIEKVLNHNHISGALPFIENPDNNYVQKILKNSRQ 539
 * * * * *

hCLASP4 VGRSLGSRMPFADAAAPFEELQHLDDGHEFSPLYKQDPSLSSEDIPLLEHYRFE 610
 hCLASP5 QSRRLSKAALSIEHNCVGNPFET-----TLVTSFFKQEDHLSDEDLFFFLADYHES 427
 hCLASP3 HSSIVGHSLEHTTSGDDACNLTFRPATLTSTNFFKQEDHLSDEDLFFFLADYHES 496
 hCLASP2 AAGRIQSRMPFADAAAPFEELQHLDDGHEFSPLYKQDPSLSSEDIPLLEHYRFE 601
 hCLASP7 ---RRIQL--DRAAGSDDACNLTFRPATLTSTNFFKQEDHLSDEDLFFFLADYHES 483
 hCLASP1 RQSKLGRARRAFVAVKSVFFEDQHLDDGHEFSPLYKQDPSLSSEDIPLLEHYRFE 599
 * * * * *

hCLASP4 --KTFDQIPGDLNITVEGVNVLNHCITSSNYPKLPPE--FNCQNTVLEVEFTPENIKY 567
 hCLASP5 SLQREVEIPGDLADEISTALHINCCITPENLVPKPF--FNFTEFKEELLEFI--TSFV 484
 hCLASP3 SLQREVEIPGDLADEISTALHINCCITPENLVPKPF--FNFTEFKEELLEFI--TSFV 553
 hCLASP2 KMAKSDMLGRLDITDNVSDNPNYNSUYPTKQFQDSSTETITLVLLEPMQCIKH 560
 hCLASP7 SLQREVEIPGDLADEISTALHINCCITPENLVPKPF--FNFTEFKEELLEFI--TSFV 540
 hCLASP1 LLSHMLTIPGLDCAVDNTEGRRNCTSSNYPKLPPE--FNCQNTVLEVEFTPENIKY 656
 * * * * *

hCLASP4 CYEFTLPHNHLAVPIQLLYDSQETFAARNIAYGVSEFDLDESIASALPIYGFHALSV 627
 hCLASP5 YVPHITVPHNHLAVPIQLLYDSQETFAARNIAYGVSEFDLDESIASALPIYGFHALSV 541
 hCLASP3 YVPHITVPHNHLAVPIQLLYDSQETFAARNIAYGVSEFDLDESIASALPIYGFHALSV 610
 hCLASP2 YVPHITVPHNHLAVPIQLLYDSQETFAARNIAYGVSEFDLDESIASALPIYGFHALSV 620
 hCLASP7 YVPHITVPHNHLAVPIQLLYDSQETFAARNIAYGVSEFDLDESIASALPIYGFHALSV 597
 hCLASP1 CREYFVPHNHLAVPIQLLYDSQETFAARNIAYGVSEFDLDESIASALPIYGFHALSV 718
 * * * * *

hCLASP4 FTTNAYVVSHHNQHEFYDEIRIHLPIHLHQHHLLETFYHVSCEINTHTTHQITVE 687
 hCLASP5 FLQEVNTAVTYRNESEDEFBEVKEHLPAHLTVNHLLLETFYHVSCEINTHTTHQITVE 595
 hCLASP3 FKEKAYVVSHHNQHEFYDEIRIHLPIHLHQHHLLETFYHVSCEINTHTTHQITVE 664
 hCLASP7 FKEKAYVVSHHNQHEFYDEIRIHLPIHLHQHHLLETFYHVSCEINTHTTHQITVE 680
 hCLASP1 FKEKAYVVSHHNQHEFYDEIRIHLPIHLHQHHLLETFYHVSCEINTHTTHQITVE 681
 * * * * *

hCLASP4 TPVGSVAVVPIKFIETITTFQCQEPGAMPHCLVNLNDAESPPQNVICRAVDCAFELIK 747
 hCLASP5 TLLGYSWPLPLLEDGHWNTSEQHIPVSNLPSGHLGYQELQNGRHYGPETKAVDGGKPLIK 655
 hCLASP3 TPVGSVAVVPIKFIETITTFQCQEPGAMPHCLVNLNDAESPPQNVICRAVDCAFELIK 721
 hCLASP7 TLLGYSWPLPLLEDGHWNTSEQHIPVSNLPSGHLGYQELQNGRHYGPETKAVDGGKPLIK 740
 hCLASP1 TPVGSVAVVPIKFIETITTFQCQEPGAMPHCLVNLNDAESPPQNVICRAVDCAFELIK 729
 * * * * *

FIG. 8 (2 of 6)

Cadherin EC motif

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hCLASP4      ENAFATKQLQP-----VQDS--NLEYSLSDEYKHHFLVGLLRETSI 1060
hCLASP5      FEMNADTAPTSP--CFGISGNNSSCSSEFQDQHIAMMTLTSEYRQQHFLTGLLFTELAA 1065
hCLASP3      FQRLTTFEASPFKEVESATPQSSSEFSTNVQDQHIAMMELVPPFQQQHYLAGIQLTTELAV 1068
hCLASP2      PMPFQKQRTLP-----YQDL--QLQSLTDEFERNHFLVGLLREYGT 1054
hCLASP7      LQCLLPPASPEPVSSSTTSLSSTFSSQAPDPHTSMELSGPFRQQHFLAGILLTELAL 1119
hCLASP1      FTRSANIPQPLTP-----SES----TQELHAIQMPESVTVNESTKHFLLIGILLREYGP 1157
                                     . . . . . * * * * *

hCLASP4      ALQDN---YHIRTNAISVHNLLIKHAFDTRIQHKNQAKIAQINVTWILLENIQL 1116
hCLASP5      ALDAEGEGISKIQFPAVCAIHCLSSHOLDPRVVKPFFVKIAALNCLAVIILDALD-- 1143
hCLASP3      ILDFDAEGLEFLERKINIVHNLSSHSDSPRLSDPQFARVAVILYHPLTITIMETVP-- 1254
hCLASP2      ALQEFR---HYRLIAISVHLNLLIKHSFDDRYASRSHQAIATYLYLPLLIENYLR 1108
hCLASP7      ALEPEAEAGAPLHKKAISAVHSLCCGHDTPRPAEATFAFVAVILYHPLTITARDTLP-- 1175
hCLASP1      AIQFDQ---YHRLALAVLENLMAKHSFDPKPEPEPRQAIANLYNINMLLINIRI 1213
                                     . . . . . * * * * *

hCLASP4      ASRDTLYSCA-----AMPN-S---AQRDEPRQGTSPANHQLLTDEKTAIGS 1160
hCLASP5      -----QL-----CDETVADETRERETSGSD----- 1162
hCLASP3      -----QLY-----DETETHNQSGHICITATIO----- 1278
hCLASP2      NVRDVSPFPNAGNTTKDSIALPA-VNPLVTPQPGSTLONSLEKDLGAGISGIASFIT 1165
hCLASP7      -----RLH-----DEAGPGQGLHIAHMLDITE 1201
hCLASP1      YLELDLYPFTWTINQISRDDELSTNGGFQSQAKKHAHSVDTSPKDYLMIAAFPSIAIS 1273
                                     . . . . .

hCLASP4      FQ-NGHGKIKREDRGGLIPEGATGFDPQCNTEGLEN-----TRQSTELAVQYNFLIQYE 1213
hCLASP5      -----EEQEGAGAINQVALAIAGNMFLNLT-----GIVLSLMLFPQYNMLNADT 1208
hCLASP3      -----YELSEGSMTSQTVAMAIAGTSVPQDTR-----PSFLLTSYSGHGHTTFAES 1324
hCLASP2      STPNINSVFNADIRGLISTISGNSLPEFNSEFSNSLDHAGQNTLQANTFQDHLQSE 1225
hCLASP7      -----GQSDIAGTINPSVAMAIAGSEFLAPGSR-----AISGPGPFAFAGCALFAES 1249
hCLASP1      -----TVNHAKRA-LASLDSPSTNEFSNEKTDNCKEFPPLALINTDEFDLQAE 1325
                                     . . . . .

hCLASP4      TRSLLMCYLYLVNHIKQVLLTYWNKVSFQELNILLLETCLEFEEHMQFNIARVHDA 1273
hCLASP5      TRNLKICFLWMFNNAQVSLIKWIADLPSTQLNRIILMLLFICVLCFFHGFQSSDKVYTG 1268
hCLASP3      TRSLLICLLWVLFNARETVLQKWFDTLSVLQLNRLDCLLYCVSCFFHGFQFVTERINSL 1384
hCLASP2      TRSLLMCFLYLKSMDDALFTYWNKASTSLMDEFTISHCLHQFQNHGFYIARVJEG 1287
hCLASP7      SRILLACVLWVLFNTRPALLQRWATDLTLPQLGRLLICLYCLAAPFHGFQFAPERINSL 1309
hCLASP1      TRSLLMCFLHMKETIYETLIAYWQRAAPSEVSDFFSILNCLQNFHGLGHENIRKIAA 1387
                                     . . . . . * * * * *

hCLASP4      KLQPHFNTLP-----YSITHALRNFQNTALRICHQSSSS----- 1111
hCLASP5      VLFPVFTFAP-----IFWALLRGRNALSHIRFPAFTTFFHLEEN----- 1211
hCLASP3      IFFPFTFMFAP-----IFFAITVIRASIRIRFIRFGLERGLVAFR----- 1311
hCLASP2      IYHIVHFP-----ITFIRFHTTIRHAILTQALINE----- 1111
hCLASP7      IFFPFTFMFAP-----IFFAITVIRASIRIRFIRFGLERGLVAFR----- 1311
hCLASP1      AAPPVLLIRNLLVIRKFTQGLAQNRSTSEFEGHGHGGLPIIKDGN----- 1342
                                     . . . . .

hCLASP4      -----FTLHRSSTTTEACIFHQAALRGNTATEYVLTLOTISFFETQCFKDLL 1059
hCLASP5      ---LFWFEEVTHWQALFKLITPAFLDCEALISGLATEARLLILINDENTQASG-ALD 1369
hCLASP3      FNIFWFPMIRWFIHTMTTPFAEIRHEALIRNATFANILCETLENTQTVS-UTE 1469
hCLASP2      -----ITRHHVYHCLAKLHRCGLIRANITATVLTATLIRLAFAPNGL 1371
hCLASP7      -----ITRHHVYHCLAKLHRCGLIRANITATVLTATLIRLAFAPNGL 1371
hCLASP1      -----ITRHHVYHCLAKLHRCGLIRANITATVLTATLIRLAFAPNGL 1371

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FIG. 8 (4 of 6)

ITAM ITAM

hCLASP4 ERTGTENVKIIQDSDFVNAKELSPFAHIQIVKRYFDIKELTEPKTEFERNNHNGREV 1869
hCLASP5 QQTGAHEVENVIKDSTFMKIPLEFNKAYIQITVEHFDDEYEMKDRVTYFENFNLRPFM 1810
hCLASP3 ERFGEDVWEVIFDSNFVCKIILIMFAIQQITAVEHFDDEYEMKDRVTYFENFNLRPFM 1930
hCLASP2 DHEGLENVEMIKDSGFVNPILLISFAAIQVTVIHFDEKELQERKTEFERSHNIRSEFM 1770
hCLASP7 ERFGEDVWEVIFDSNFVCKIILISFAAIQVTVIHFDEYEMKDRVTYFENFNGLRTPFL 1851
hCLASP1 DHEGADNVKIIQDSNKNVNPILLIPFAAIQVTVIHFDEKELQERKTEFERSHNIRSEFM 1972

ITAM DCC motif

hCLASP4 FEAPYTLGGHKGQGEIEFQQYRTILITNSSEAVKFIIFINCEQQINLRPIDGATDEIKD 1859
hCLASP5 YTIPTFTLEGGHPRGELHEQYFRNI/LTINHAFFIIPFISVIQKEEFVLTPIEVAIEDMK 1870
hCLASP3 YCTPTFTLEGGHAGSEIHEQYFRKTLITINHAFFIIPFISVNYTHKEEIIITPIEVAIEDMQ 1992
hCLASP2 FEMPTFTCGHKGQSSVEEQYRRTILTAIHCFPMVHKPIFMYQHHTDNLNPIEVAIDEM 1830
hCLASP7 FCTPTFTLEGGHAGSEIPEQYFRKTLITINHAFFIIPFISVNYTHKEEIIITPIEVAIEDMQ 1911
hCLASP1 FETPTFTLSSGKHGSSVAEQYRRTILITINHLFPMVHKPIQVISQSSTELNPIEVAIDEMBR 2032

Coiled-coil

hCLASP4 RTAELQRLSSSIDVLAJLLEKLGVWSVCVNADELAYAFINDSQACKYPRHKVSELR 1919
hCLASP5 ETLQLAVAINTEPPFAKMLMVLGVWSVCVNADELAYAFINDSQACKYPRHKVSELR 1930
hCLASP3 RTQELAFATHIDPADPMLMVLGVWSVCVNADELAYAFINDSQACKYPRHKVSELR 2052
hCLASP2 FVAELRQLSSAEVDMLKMLLKLGVWSVCVNADELAYAFINDSQACKYPRHKVSELR 1890
hCLASP7 FTEELAFATEIDPPDAFHLQMLLGVWSVCVNADELAYAFINDSQACKYPRHKVSELR 1971
hCLASP1 FVSELNLQDITMELVDMLSLQHLGLGVWSVCVNADELAYAFINDSQACKYPRHKVSELR 2092

Coiled-coil

hCLASP4 DMFRKFIQACSIALELNERLIKELQVYHHEGLKIFRIMVPELSDIHEQILQEDTMHSP 1979
hCLASP5 LCFKEEFIMRQGEAVEFNELITAIQREYQDELAPNINLFAENLRPMIERRIPELYAPIFR 1990
hCLASP3 LCFKEDFTKIDEDALRNKSLIGPVQREYQDELQVSSP----- 2090
hCLASP2 EVFFQFVHADGIALANERLIKEIDLEYQDEMKANYFEMAKELSEIMHEQICILHEKTS- 1949
hCLASP7 LCFKDFCKKIDEDALRNKALIGPVQKEYHRELENYCKLRKALQPLLTQRLPQIMATP- 2030
hCLASP1 EIERQFADADGALDYNERLIKEIDLEYQEELRHYKDMLSSELSTVMNEQITGFDDLSKR 2152

PTC ligand

hCLASP4 WM3NTLHVPCVLSGTS SDRGIGSFSAEV-- 2018
hCLASP5 VESQKRDSFHKNSFRFQETQLSQG----- 2015
hCLASP3 -----
hCLASP2 VLPNSLHIFNAISGTHSTNVHGMSSSSVY 1940
hCLASP7 --PGLRNSINP/SFRPADL----- 2017
hCLASP1 GVDQTCRTRVISHATPALPTVSISSCAE-- 2140

FIG. 8 (6 of 6)